

## SEQUENCE LISTING

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01200 Corynebacterium glutamicum GENES ENCODING  
 METABOLIC PATHWAY PROTEINS

01300 BGI-121CP2

01400 VS 09,746,660

01410 09-12-22

01500 09-06-041

01510 09-06-12

01600 09-06-124

01610 09-06-12

01700 09-14-101

01710 09-06-12

01800 09-14-101

01810 09-06-12

01900 09-14-101

01910 09-06-12

02000 09-18-971

02010 09-06-12

02100 LE 19-01480.9

02110 09-06-12

02200 123

02300 Patent In Vers. 2.0

02400 1

02410 1-40

02420 CNA

02430 Corynebacterium glutamicum

02500

02510 CDS

02520 (363)1..(1676)

04000 1

gagaaaattgt gtgagaaaat gcatgcagaa aaaggaaaagt tcgggccaag atgggtgttt 60

ctgtatcagg atgatgggat ctttgacaga tgggtatgag acaaataccc gagagttgtt 120

aattctaac aatggaaaag taacattgag agatgattta taccatcctg caccatttag 180

agtgggacta gtcatacccc cataacccta gctgtaagca atcgatttca aatcagttgg 240

aaaaagtcaa gaaaattacc cgagaattaa tttataaccac acagtctatt gcaatagacc 300  
 aaggtgttca gtaggggtgca tgggagaaga atttctaatt aaaaactctt aaggacctcc 360  
 aa atg cca aag tac gac aat tcc aat gct gac cag tgg ggc ttt gaa 407  
 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu  
 1 5 10 15  
 acc cgc tcc att cac gca ggc cag tca gta gac gca cag acc agc gca 455  
 Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala  
 20 25 30  
 cga aac ctt cgg atc tac caa tcc acc gct ttc gtg ttc gac tcc gct 503  
 Arg Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala  
 35 40 45  
 gag cac ggc aag cag cgt ttc gca ctt gag gat cta ggc cct gtt tac 551  
 Glu His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr  
 50 55 60  
 tcc cgc ctg acc aac cca acc gtt gag gct ttg gaa aac cgc atc gct 599  
 Ser Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala  
 65 70 75  
 tcc ctg gaa ggt ggc gtc cac gct gta ggc ttc tcc tcc gga cag ggc 647  
 Ser Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala  
 80 85 90 95  
 ggc acc acc aac ggc att ttg aac ctg gca ggc ggc ggc gac cac atc 695  
 Ala Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile  
 100 105 110  
 gtc acc tcc cca cgc ctg tac ggt ggc acc gac act cca ttc ctg atc 743  
 Val Thr Ser Pro Arg Leu Tyr Gly Gly Thr Gln Thr Leu Phe Leu Ile  
 115 120 125  
 act ctt aac cgc ctg ggt atc gat gtt tcc ttc gtg gaa aac ccc gac 791  
 Thr Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp  
 130 135 140  
 gag cct gag tcc tgg cag gca gcc gtt cag cca aac acc aaa gca ttc 839  
 Asp Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe  
 145 150 155  
 ttc ggc gag act ttc gcc aac cca cag gca gac gtc ctg gat att cct 887  
 Phe Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro  
 160 165 170 175  
 ggc ctg gct gaa gtt cgc cac cgc aac agc gtt cca ctg atc atc gac 935  
 Ala Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp  
 180 185 190  
 aac acc atc gct acc gca ggc ctg ctg cgc cgc ctg cag ctg ggc gca 983  
 Asn Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Gln Leu Gly Ala  
 195 200 205  
 gag gtt gtc gtc gct tcc ctg acc aag ttc ttc acc gcc aac ggc tcc 1031  
 Asp Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser  
 210 215 220

gga ctg ggc ggc gtg ctt atc gac ggc gga aag ttc gat tgg act gtc 1079  
 Gly Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val  
 215 230 235

gaa aag gat gga aag cca gta ttc ccc tac ttc gtc act cca gat gct 1127  
 Glu Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala  
 240 245 250 255

gct tac cac gga ttg aag tac gca gat ctt ggt gca cca gcc ttc ggc 1175  
 Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly  
 260 265 270

ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc ctc tcc 1223  
 Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser  
 275 280 285

gca tcc aac gca tgg gct gca gtc cag gcc atc gac acc ctt tcc ctg 1291  
 Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu Ser Leu  
 290 295 300

cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa ttc ctc 1319  
 Arg Ile Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Gln Phe Leu  
 305 310 315

aac aac cac gag aag ctg gaa aag gtt aac ttc gca gcc ctg aag gat 1367  
 Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp  
 320 325 330 335

tcc ctt tgg tac gca acc aag gaa aag ctt gcc ctg aag tac acc gcc 1415  
 Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly  
 340 345 350

tcc att ctc aac tcc aag atc aag gcc gcc aag gat aag gct tgg gca 1463  
 Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala  
 355 360 365

ttt atc gac gcc ctg aag cta cac ttc aac ctt gca aac atc cgc gat 1511  
 Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp  
 370 375 380

gtt gcc tcc ctc gtt gtt cac gca gaa acc acc acc cat tca aag tcc 1559  
 Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser  
 385 390 395

gac gaa gct gcc ctg gca gcc gag gcc gtt acc cag tcc acc gcc gcc 1607  
 Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg  
 400 405 410 415

aag tcc gtt gcc atc aag acc att gat gat atc atc gct gac ctc gaa 1655  
 Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu  
 420 425 430

gcc gcc ttt gct gca atc tag cttttatatag aactaaccca gtgcttaaag 1706  
 Gly Gly Phe Ala Ala Ile  
 435

cgttgggttt ttctttttca gactgtgag aatgcataact agatagaca gagctgtcca 1756

tatacaactgg accgaagtttt agtcttgtcc accagaacaa gccgtgttatt ttcattgccc 1826

cccctggccc ttca 1840

02108-2  
 02110-437  
 02120-PET  
 02130-Corynebacterium glutamicum

0400-1  
 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr  
 1 5 10 15  
 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg  
 20 25 30  
 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu  
 35 40 45  
 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser  
 50 55 60  
 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser  
 65 70 75 80  
 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala  
 85 90 95  
 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val  
 100 105 110  
 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr  
 115 120 125  
 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp  
 130 135 140  
 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe  
 145 150 155 160  
 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro Ala  
 165 170 175  
 Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp Asn  
 180 185 190  
 Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala Asp  
 195 200 205  
 Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser Gly  
 210 215 220  
 Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val Glu  
 225 230 235 240  
 Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala Ala  
 245 250 255  
 Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu  
 260 265 270  
 Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala  
 275 280 285



Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg  
 290 295 300

Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn  
 305 310 315 320

Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser  
 325 330 335

Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser  
 340 345 350

Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe  
 355 360 365

Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val  
 370 375 380

Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser Asp  
 385 390 395 400

Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu  
 405 410 415

Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly  
 420 425 430

Gly Phe Ala Ala Ile  
 435

410 - 3

411 - 1495

412 - DNA

413 - *Corynebacterium glutamicum*

414 -

415 - GDS

416 - (287)...1264)

417 - 3

ataggtttt ctcagcggaa acggttggc tctcagcact ttcacccgaa cagcctgcaa 60

gaagtcggac ggctaacagg gctgggattg tctcgaactt caattcgggc tcttcttag 120

caataggttc gtagaaaagt ttactagcct agagagtatg cgatttctg aactogaaga 180

attgaagaat cgcggacct tgaaatggac cgggtttcca gaagacgtg tctctttgtg 240

ggttgcggaa atgattttg gcacctggc gcagttgaag gaagct atg gca gat 295  
 Met Ala Asp  
 1

ccc gtt gag cgc gag gtc ttc gga tac cca cca gat gct act ggg ttg 343  
 Ala Val Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala Thr Gly Leu  
 5 10 15

aat gat ggc ttg act gga ttc tac gag cgt cgc tat ggg ttt ggc cca 391  
 Asn Asp Ala Leu Thr Gly Phe Tyr Glu Arg Tyr Gly Phe Gly Pro  
 20 25 30 35

aat ccc gaa agt gtt ttc gcc att ccc gat gtg gtt cgt ggc ctg aag 439  
 Asn Pro Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg Gly Leu Lys  
 40 45 50

ctt gcc att gag cat ttc act aag cct ggt tgg gcc atc att gtg ccc 487  
 Leu Ala Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile Ile Val Pro  
 55 60 65

ttg cct gca tac ccc cct ttc att gag tgg cct aag gtg act ggt cgt 525  
 Leu Pro Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val Thr Gly Arg  
 70 75 80

cag gcc atc tac att gat gcc cat gag tac gat ttg aag gaa att gag 583  
 Gln Ala Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys Glu Ile Glu  
 85 90 95

ang gcc ttc gct gag ggt ccc gga tca ctg ttg ttc tcc att cca ccc 631  
 Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys Asn Pro His  
 100 105 110 115

aac cca ctg gcc aag gtc ttc tct gaa gag tac acc ccc gag ctg acc 679  
 Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg Glu Leu Thr  
 120 125 130

gat att gcc gcc aag tac gat gcc ccc atc atc gcc gat gag atc ccc 727  
 Asp Ile Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp Glu Ile His  
 135 140 145

cag cca ctg gtc ttc gaa gcc acc cat gtg gcc gcc gat ggt ctt tct 775  
 Ala Pro Leu Val Tyr Glu Gly Thr His Val Val Ala Ala Gly Val Ser  
 150 155 160

gag aac gct gca aac act tgc atc aac atc acc gca act tct aag gcc 823  
 Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr Ser Lys Ala  
 165 170 175

tgg aac act gct gat ttg aag tgc gct cag atc ttc ttc agt aat gaa 871  
 Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe Ser Asn Glu  
 180 185 190 195

acc gat gtc aag gcc tgg aag aat ttg tgg gat att acc cgt gac gat 919  
 Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr Arg Asp Gly  
 200 205 210

gtg tcc atc ctt gga ttg atc gct gcc gag aca gtg tac aac gag gcc 967  
 Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr Asn Glu Gly  
 215 220 225

gaa gaa ttc ctt gat gag tca att cag att ctc aag gac aac cgt gac 1015  
 Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp Asn Arg Asp  
 230 235 240

att gcc gct gct gaa ctg gaa aag ctt gcc ctg aag gtc tac gca ccc 1063  
 Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val Tyr Ala Pro  
 245 250 255

gac tcc act tat ttg atg tgg ttg gac ttc cct gcc acc aag atc gaa 1111  
 Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr Lys Ile Glu  
 260 265 270 275

gag ggg cct tct aaa att ctt cgt gag gag ggt aag gtc atg ctg aat 1159  
 Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val Met Leu Asn  
 280 285 290

gat ggc gca ggt ttt ggt ggt ttc acc acc tgc gct cgt ctt aat ttt 1207  
 Asp Gly Ala Ala Phe Gly Gly Phe Thr Thr Cys Ala Arg Leu Asn Phe  
 295 300 305

ggg tgt tcc aga gag acc ctt gag gag ggg ctg cgc cgt atc gcc agc 1255  
 Ala Cys Ser Arg Glu Thr Leu Glu Glu Gly Leu Arg Arg Ile Ala Ser  
 310 315 320

gtg ttg taa ataataagta aaaagtctgt cctgattact tctttgatgc 1304  
 Val Leu  
 325

tgttttcacat gttcttcogga gctggaaacc tctctctccc gctgatgctt ggattgtcgg 1364

caggaaccaa ctatctacca gctatcttag gattcttagc aacgagcttt ctgctccggg 1424

tgtctgggat tatctgggtg ggtctgtcgg gagaacatgt caaggacatg gctctctgtg 1484

ccgtaagat c 1495

210: 4  
 211: 125  
 212: 15T  
 213: Corynebacterium glutamicum

400: 4  
 Met Ala Asp Ala Val Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala  
 1 5 10 15

Thr Gly Leu Asn Asp Ala Leu Thr Gly Phe Tyr Glu Arg Arg Tyr Gly  
 20 25 30

Phe Gly Pro Asn Pro Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg  
 35 40 45

Gly Leu Lys Leu Ala Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile  
 50 55 60

Ile Val Pro Leu Pro Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val  
 65 70 75 80

Thr Gly Arg Gln Ala Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys  
 85 90 95

Glu Ile Glu Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys  
 100 105 110

Asn Pro His Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg  
 115 120 125

Glu Leu Thr Asp Ile Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp  
 130 135 140

Glu Ile His Ala Pro Leu Val Tyr Glu Gly Thr His Val Val Ala Ala  
 145 150 155 160

Gly Val Ser Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr  
 165 170 175  
 Ser Lys Ala Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe  
 180 185 190  
 Ser Asn Glu Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr  
 195 200 205  
 Arg Asp Gly Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr  
 210 215 220  
 Asn Glu Gly Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp  
 225 230 235 240  
 Asn Arg Asp Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val  
 245 250 255  
 Tyr Ala Pro Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr  
 260 265 270  
 Lys Ile Glu Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val  
 275 280 285  
 Met Leu Asn Asp Gly Ala Ala Phe Gly Gly Phe Thr Thr Cys Ala Arg  
 290 295 300  
 Leu Asn Phe Ala Cys Ser Arg Glu Thr Leu Glu Glu Gly Leu Arg Arg  
 305 310 315 320  
 Ile Ala Ser Val Leu  
 325

&lt;210&gt; 1

&lt;211&gt; 1033

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1006)

&lt;400&gt; 5

gtgcggatcg ggtatccgcg ctacacttag aggtgtaga gatcatgagt ttccacgaac 60  
 tgtaacgcag gattcaccaa tcaatgaaag gtgcaccgac atg agc act gaa gac 115  
 Met Ser Thr Glu Asp  
 1 5  
 att gtc gtc gta gca gta gat ggc tgg gac gcc tca aaa caa gct gtt 163  
 Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val  
 10 15 20  
 cgg tgg gct gca aat acc gcc aac aaa cgt ggc att tca ctt cgc ttg 211  
 Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu  
 25 30 35  
 gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt 259  
 Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val  
 40 45 50

cca cca caa gag att ttc gat gac etc cag gcc gaa gcc ctg gaa aag Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys 55 60 65	307
att aac gaa gcc agt gac atc gcc cac gag gta gag cca gaa atc aag Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys 70 75 80 85	355
atc ggg cac acc atc ggt gaa gcc agt ccc atc gac atg ctg ctg gaa Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu 90 95 100	403
atg tct ccc gat gcc aca atg atc gtc atg ggt tcc aga gga etc ggc Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly 105 110 115	451
gga etc tcc gga atg gtc atg gcc tcc gtc tcc ggt gca ggc etc agc Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser 120 125 130	499
cac gca aag tct cca gtc gtt gtt gtc agt gaa gac agc gca gtc aac His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn 135 140 145	547
gaa gac agc aag cac gcc cca gtc gtc gtc ggt ggc cat gcc tcc gaa Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu 150 155 160 165	595
gtc tcc cca cag gca acc gaa cac gca ttc ggt gaa tct gaa gct agt Val Ser Gln Gln Ala Thr Glu Cys Ala Phe Ala Glu Ala Glu Ala Arg 170 175 180	643
ggc gcc gaa etc gtc gca ttc cac acc tgg atc gac atg cag cca cag Gly Ala Glu Leu Val Ala Val His Thr Cys Met Asp Met Gln Val Gln 185 190 195	691
gca tca att gca ggt att gca gct gct caa cag cag tgg gat caa ggc Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val 200 205 210	739
gaa agt cag caa acc gac atg ctg atc gaa agc etc gca cca ctg ggc Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Asn Leu Ala Pro Leu Val 215 220 225	787
gaa aag cac cca agt gta acc gtc aag aag atc atc acc agt gac agc Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg 230 235 240 245	835
cca gtt ctc gca etc gca gaa gca tct gaa aac ggc cag etc cta gtc Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val 250 255 260	883
gtt ggt tcc cat ggt agt gcc aga ttc aag ggc atg etc att agc tcc Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser 265 270 275	931
acc tcc agc gca ctg ctg caa tcc gca cag tgt cca atg atg atg gtc Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val 280 285 290	979

cgc cca cct gag aag att aag aag tag tttcttttaa gtttcgatgc cccgggtt 1033  
 Arg Pro Pro Glu Lys Ile Lys Lys  
 295 300

02100: 6  
 02110: 301  
 02120: PRT  
 02130: Corynebacterium glutamicum

04000: 6  
 Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala  
 1 5 10 15  
 Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly  
 20 25 30  
 Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr  
 35 40 45  
 Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala  
 50 55 60  
 Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val  
 65 70 75 80  
 Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile  
 85 90 95  
 Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly  
 100 105 110  
 Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser  
 115 120 125  
 Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu  
 130 135 140  
 Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly  
 145 150 155 160  
 Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala  
 165 170 175  
 Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met  
 180 185 190  
 Asp Met Glu Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Glu  
 195 200 205  
 Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg  
 210 215 220  
 Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile  
 225 230 235 240  
 Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn  
 245 250 255  
 Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly  
 260 265 270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys  
 275 280 285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys  
 290 295 300

02160: 7  
 02110: 948  
 02120: DNA  
 02130: Corynebacterium glutamicum

02200:  
 02210: CDS  
 02220: (101)..  
 02230: PKA02229

02400: 7  
 121ggtttaa cagagaccac cgcgtgtctt gggtcgacgc ctctggcgat cccaccgcac 60  
 122cttggga gatitttgggt ctacaatagc gaggggtgaat ttg acc atc ccc ttt 115  
 Leu Thr Ile Pro Phe  
 1 5  
 123aaa ggc cac gcc acc gaa aac gac ttc atc atc atc ccc gat gag 163  
 Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu  
 10 15 20  
 124ggc cgc cta gat tta acc cca gaa atg gtg gtc acg ctg ttt gac 211  
 Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp  
 25 30 35  
 125ggc cgc ggc ggg atc ggt gct gat ggt atc ccc gcc ctg gtt aaa gct 259  
 Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala  
 40 45 50  
 126gaa gac gta gaa ggc tcc acg gtc gac cca tgc ctg tgg ttc atg gat 307  
 Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp  
 55 60 65  
 127aac cgc aac gcc gat gaa tct ttg gct gaa atg tcc ggc aat ggt gtg 355  
 Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val  
 70 75 80 85  
 128cgc ctg ttc ggc cac tgg ctg tac tcc cgc ggt ctt gtt gat aat acg 403  
 Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr  
 90 95 100  
 129age ttt gat atc ggt acc cgc gcc ggt gtc cgc cac gtt gat att ttg 451  
 Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu  
 105 110 115  
 130cag gca gat caa cat tct ggc cag gtc cgc gtt gat atg ggc atc cct 499  
 Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro  
 120 125 130  
 131gac gtc acg gga tta tcc acc tgc gac atc aac ggc caa gta ttc gct 547  
 Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn Gly Gln Val Phe Ala  
 135 140 145

ggc ctt ggc gtt gat atg ggt aac cca cac cta ggc tgc gtt gtg cgg 595  
 Gly Leu Gly Val Asp Met Gly Asn Pro His Leu Ala Cys Val Val Pro  
 150 155 160 165  
 ggc tta agt ggc tgg gct ctt gcc gat atg gaa ctg cgc gca cct acg 643  
 Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu Leu Arg Ala Pro Thr  
 170 175 180  
 ttt gat cag gaa ttc ttc ccc cac ggt gtg aac gta gaa atc gtc aca 691  
 Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn Val Glu Ile Val Thr  
 185 190 195  
 gaa tta gaa gat gac gca gta tgg atg cgc gtg tgg gaa cgc gga gtg 739  
 Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val  
 200 205 210  
 ggc gaa acc cgc tcc tgt ggc aag gga acc gtu gct gaa ggc tgt gct 787  
 Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val Ala Ala Ala Cys Ala  
 215 220 225  
 gct tta gct gat gct gga tgg gga gaa ggc aca gct aca gtg tgc gtt 835  
 Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val  
 230 235 240 245  
 cca cgt ggg gaa gta gaa gtr cag atc ttt gac gac gac tcc aca ctc 883  
 Pro Arg Gly Glu Val Glu Val Glu Ile Phe Asp Asp Gly Ser Thr Leu  
 250 255 260  
 acc ggc ccc acc gcc atc atc gaa ctc ggt gag gtg cag atc 925  
 Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu Val Glu Ile  
 265 270 275  
 taagattcgc gattgtagtt cgg 948

&lt;210&gt; :

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; :

Leu Thr Ile Pro Phe Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile  
 1 5 10 15  
 Ile Ile Pro Asp Glu Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val  
 20 25 30  
 Val Thr Leu Cys Asp Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu  
 35 40 45  
 Arg Val Val Lys Ala Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser  
 50 55 60  
 Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met  
 65 70 75 80  
 Cys Gly Asn Gly Val Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly  
 85 90 95  
 Leu Val Asp Asn Thr Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg  
 100 105 110



His Val Asp Ile Leu Gln Ala Asp Gln His Ser Ala Gln Val Arg Val  
 115 120 125  
 Asp Met Gly Ile Pro Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn  
 130 135 140  
 Gly Gln Val Phe Ala Gly Leu Gly Val Asp Met Gly Asn Pro His Leu  
 145 150 155 160  
 Ala Cys Val Val Pro Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu  
 165 170 175  
 Leu Arg Ala Pro Thr Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn  
 180 185 190  
 Val Glu Ile Val Thr Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val  
 195 200 205  
 Trp Glu Arg Gly Val Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val  
 210 215 220  
 Ala Ala Ala Cys Ala Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr  
 225 230 235 240  
 Ala Lys Val Cys Val Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp  
 245 250 255  
 Asp Gly Ser Thr Leu Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu  
 260 265 270  
 Val Gln Ile  
 275

0110 - 9  
 0111 - 1491  
 0112 - DNA  
 0113 - *Corynebacterium glutamicum*

0120 -  
 0121 - GDS  
 0122 - (1010) .. (1468)  
 0123 - EXS02970

0400 - 9  
 aacagacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60  
 tattttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115  
 Leu Ala Leu Lys Gly  
 1 5  
 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa goa 163  
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
 10 15 20  
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc ggc cac gtt ttc 211  
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
 25 30 35  
 cac tcc tgg tcc ggc cag gac aaa atc agc ccc aaa gta tgg gca gct 259

His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
40 45 50	
gac gaa ggt tcc acg ctg tac gac ttc gac ggc aac ggc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc tgg gca aac ata ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80	
tta gtt gag gag atc cag cgc caa gca tcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
cag gac ttc ggc aat gat gtg cgc tcc tat gtt got gca aag atc gtc	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tgg atg gac cgt ggc gaa ttc tcc cac atg ttc ttc aac aac gag ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gac tac ggc atc gag cac tcc atc cgc atg gtt cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc cgc tat cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc cgc atg atc ctc acc ggc gaa cac cgc tat ctg ggc aac cct acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc aac caa gat atc tac cac ttc tgg caa caa ttc ctt cac caa tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa caa tcc gaa cgc gca ctg aat	739
Ser Phe Phe Ala Thr Thr Gln Gln Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc ggc ttt gaa ggt got ggc atg atc gca ggc	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag caa gtg gtg gga tca tca gaa atc atc ctg caa caa	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca cgt tac tta aat ggc gtg cgc gaa ctt tcc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aac	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt got tac gag cat got gcc gac gat ttc cag caa gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	

280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctg ggt ggc atc 1027  
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
 305 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075  
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Gln Ala Tyr Ser  
 310 315 320 325

ggc gga ctg acc tac tcc gga cac caa ctt gca gta gca ccc gcc aag 1123  
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
 330 335 340

gca agc ctg gag att tac ggc gaa gga gag atc att cca cga gta gct 1171  
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
 345 350 355

aga att agt gat gaa ctg atc gaa cct cgc ctt cgt gaa cca ggc gaa 1219  
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
 360 365 370

gaa aac ctg gag att gct gac gtc ggc ggc atc gga ttc tcc tgg gca 1267  
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
 375 380 385

ctg gag ttc aac gca gac gcc act gcc atg gcc gcc gac gcc gca gaa 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

ttc gag att ctc ggc gag tgg ccg atg acc tcc ggc aac cga ttc cac 1363  
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
 410 415 420

acc gcc ccc ctg ctg acc acc act gat gac gaa ttg gta gca ctg ctg 1411  
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
 425 430 435

gac ccg gta gaa gcc gca gcc caa gct gtc gag ctg acc ttc gct ggc 1469  
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly  
 440 445 450

ggc ttg ttc taagttttct agataacaag gcc 1491  
 Ala Leu Phe  
 455

G110 - 10

G111 - 456

G112 - PRT

G113 - *Corynebacterium glutamicum*

G400 - 10

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe  
 1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Gly Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser  
405 410 415

Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu  
420 425 430

Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu  
435 440 445

Leu Thr Phe Ala Gly Ala Leu Phe  
450 455

C10 - 11  
C11 - 1330  
C12 - DNA  
C13 - *Corynebacterium glutamicum*

C20 -  
C21 - CDS  
C22 - 1010... 1330  
C23 - PRXA01019

C100 - 11  
accacacaaa acagcgcgttc acgtgcctaaa gcagctcggc ttgatctagg gtgcggtgag 60

ttattaaag acctcataat attctggggg gtgaactggt ttg gca ttg aag ggt 115  
Leu Ala Leu Lys Gly  
1 5

tac acc aac tit gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
10 15 20

aaa aac gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
Lys Gln Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
25 30 35

tac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
40 45 50

gac gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
55 60 65

atg ggt tcc caa ctt gtc tgg gca aac tta ggc cac aac aac cct cga 355  
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451

Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val	Ala	Ala	Lys	Ile	Val	
			106					110					115			
tcc	atg	gac	cgt	ggc	gaa	ttc	tcc	cac	gtg	ttt	ttc	acc	aac	ggc	ggc	499
Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe	Phe	Thr	Asn	Gly	Gly	
		120					125				130					
gac	gac	gac	atc	gag	cac	tcc	atc	cgc	atg	gct	cgc	ctg	cac	acc	gga	547
Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala	Arg	Leu	His	Thr	Gly	
	135					140				145						
cgc	aac	aaa	att	ctg	tcc	gca	tac	cgc	agg	tac	cac	ggc	gca	acc	gga	595
Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr	His	Gly	Ala	Thr	Gly	
150					155				160					165		
tcc	gag	atg	atg	ctc	acc	cgc	gaa	cac	cgc	cgc	ctg	ggc	aac	ccc	acc	643
Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg	Leu	Gly	Asn	Pro	Thr	
			170					175						180		
acc	gac	cca	gat	atc	tac	cac	tcc	tgg	gga	cca	ttc	ctg	cac	ccc	tcc	691
Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser	
		185						190					195			
tca	ttc	tcc	gac	acc	acc	caa	gaa	gaa	gaa	tgc	gaa	cgc	gca	ctc	aac	739
Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys	
	200					205				210						
cac	ctg	gaa	gat	gtc	atc	cgc	tcc	caa	ggt	gct	ggc	atg	atc	gca	gac	787
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala	
	215				220				225							
atc	gac	cgc	gag	cca	gtg	ctg	ggt	tcc	tca	gga	atc	atc	ctg	ccc	cca	835
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro	
230				235					240				245			
gca	ggt	tac	tta	aac	ggc	ctg	cgc	gaa	ctt	tgc	aac	aag	cac	ggc	atc	883
Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile	
			250					255					260			
ctc	tcc	atc	gac	gac	gaa	gtc	atg	gtc	gga	tcc	gga	cgc	acc	ggc	aaa	931
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys	
		265					270					275				
ctg	tcc	gct	tac	gag	cat	gct	ggc	gac	gat	tcc	cag	cca	gac	atc	atc	979
Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile	
	280					285					290					
acc	tcc	gac	aag	ggt	gtt	aac	gca	ggt	tac	gac	cca	ctc	ggt	ggc	atc	1027
Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	Pro	Leu	Gly	Gly	Ile	
	295					300				305						
gtg	atg	acc	caa	tca	atc	cgc	gat	acc	tcc	gga	cca	gag	gca	tac	tcc	1075
Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser	
310					315					320				325		
ggc	gga	ctc	acc	tac	tcc	gga	cac	cca	ctt	gca	gta	gca	ccc	gct	aag	1123
Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys	
			330					335					340			
gca	gag	ctg	gag	att	tac	gag	gaa	gga	gag	atc	att	cca	cgc	gta	gct	1171
Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	Ile	Pro	Arg	Val	Ala	



Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 His Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365  
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
 370 375 380  
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
 385 390 395 400  
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly  
 405 410

#210 - 13

#211 - 793

#212 - DNA

#213 - *Corynebacterium glutamicum*

#220 -

#221 - CDS

#222 - (101)...(769)

#223 - EXC02390

#400 - 13

gctggtggtg ctgaaccata cgttggaact ccaactgctg ttgataccgc caagatgttt 60

ggcgcgcagg atctgttagc tcgtttcag tcattaggccg gtc gag tgg acc gct 115  
 Val Glu Trp Thr Ala  
 1 5

ttt ggc acc ctg att ctg ctg aat ttg gtc ggc agt tta tcc ccg ggg 163



Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly	
10 15 20	
cct gat acc ttt ttc ctc ctc cgc tta gcc acc cgc tcc aga ggc cac	211
Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His	
25 30 35	
ggg atc gat ggc gtc gcc ggc atc gtc acc gga ctc acg gtg tgg gtg	259
Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val	
40 45 50	
acg ctg acg gtc gtg gga gaa ggc ggc ctg ctc acc act tat cag tgg	307
Thr Leu Thr Val Val Gly Ala Ala Leu Leu Thr Thr Tyr Pro Ser	
55 60 65	
att ctc gga atc atc cag ctc gtc ggc ggc acc tac cta agc ttc att	355
Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile	
70 75 80	
ggg tac aag ctg ctg cgc tgg cgc tgg aga gag ctc atc gac gcc cgc	403
Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg	
85 90 95 100	
cag ttc cgt ctc aac gcc gat gcc cga cct atc cag gat gag gta gaa	451
Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu	
105 110 115	
aca ctg gga acc cgc act cag gta tat cga caa ggt ctg gcc acc aac	499
Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn	
120 125 130	
ctg tca acc cgt aac gtt gtc acg tac ttc gag gca att ctg gat cag	547
Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro	
135 140 145	
ctg atg caa ggc cac caa caa cgc gtc ctg gag ctc tct atc atc gtg	595
Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val	
150 155 160 165	
ggg att caa gtg cag acc ttt gtt acc ttc cct gat gtg tgg ctc att	643
Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile	
170 175 180	
gtc tct aag gag cgt gtc cgc aaa gca atg ctg cgt gca ggt ccc tgg	691
Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp	
185 190 195	
ttt gac ctg att ggt ggc gtt gtc ttc ctc gtt gtg ggt gtg act ctg	739
Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu	
200 205 210	
ctg tat gaa ggc ctg acc ggt tta ctc ggc taaaggcata aaaaatgggt	789
Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly	
215 220	
acc	792

(210): 14  
 (211): 223  
 (212): PRT

02130 Corynebacterium glutamicum

04000 14

Val Glu Trp Thr Ala Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly  
1 5 10 15

Ser Leu Ser Pro Gly Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr  
20 25 30

Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly  
35 40 45

Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu  
50 55 60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr  
65 70 75 80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu  
85 90 95

Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile  
100 105 110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln  
115 120 125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala  
130 135 140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala  
145 150 155 160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser  
165 170 175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu  
180 185 190

Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val  
195 200 205

Val Gly Val Thr Leu Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly  
210 215 220

02100 15

02110 897

02120 DNA

02130 Corynebacterium glutamicum

02200

02210 CDS

02220 (101)..(874)

02230 E0001796

04000 15

atgttaactgg atcaggtggga aatgcccgsa aaagtggcgg cgggtggcga ggggatggcgg 60

ttggtggcgg atcgggtggcc tgcactagt cgggtctcttc ttg ctc ctt ggc ggt 115  
Leu Leu Leu Gly Gly

															1	5	
aac	cct	goc	gag	atc	gac	cag	gtt	tta	ggt	ggc	gat	caa	acc	cag	atc		163
Asn	Pro	Ala	Glu	Ile	Asp	Gln	Val	Leu	Gly	Gly	Asp	Gln	Thr	Gln	Ile		
				10					15					20			
gag	tct	gga	gag	tcc	acc	gga	goc	ggc	gac	ttt	gat	cac	tgc	caa	acc		211
Glu	Ser	Gly	Glu	Ser	Thr	Gly	Ala	Gly	Asp	Phe	Asp	His	Cys	Gln	Thr		
			25					30					35				
ggt	gca	gat	goc	aac	goc	agt	gat	gat	tgt	ggc	gtt	tac	tac	acc	tca		259
Gly	Ala	Asp	Ala	Asn	Ala	Ser	Asp	Asp	Cys	Arg	Leu	Tyr	Tyr	Thr	Ser		
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ttc	tcc	gac	aat	gaa	atg	tgg	cag	act	tgg	gtt	cga	gct	cag	gct	ggt		307
Phe	Ser	Val	Asn	Glu	Met	Trp	Gln	Thr	Leu	Leu	Pro	Ala	Gln	Ala	Gly		
	55				60					65							
atc	gaa	tac	acc	gag	cag	acc	tgg	act	gtt	tcc	aaa	aac	tac	acc	caa		355
Ile	Gln	Tyr	Thr	Glu	Pro	Thr	Leu	Thr	Leu	Phe	Lys	Asn	Ser	Thr	Gln		
	70				75				80						85		
aat	ggc	tac	ggt	ttc	gat	tct	gag	tcc	act	ggc	cag	ttt	tac	tgt	cag		403
Phe	Gly	Cys	Gly	Phe	Ala	Ser	Ala	Ser	Thr	Gly	Pro	Phe	Tyr	Cys	Pro		
				90				95						100			
tca	gac	cac	gat	gat	tat	ttc	gac	tgg	act	tcc	tcc	gat	cag	arg	cgt		451
Ser	Asp	Gln	Asp	Ala	Tyr	Phe	Asp	Leu	Thr	Phe	Phe	Asp	Gln	Met	Arg		
			105					110					115				
cag	ttc	gct	gca	gaa	aac	goc	cag	gtt	goc	cag	atg	tac	acc	gtg	goc		499
Gln	Phe	Gly	Ala	Glu	Asn	Ala	Pro	Leu	Ala	Gln	Met	Tyr	Ile	Val	Ala		
		120					125					130					
caa	gag	tac	ggc	cac	cac	gtc	caa	aac	cgc	gag	ggc	aca	cgc	gga	cgc		547
His	Gln	Tyr	Gly	His	His	Val	Gln	Asn	Leu	Glu	Gly	Thr	Leu	Gly	Leu		
	135					14					145						
tcc	aat	tac	aac	gat	cag	ggc	gct	gat	tcc	aac	goc	gtc	arg	atc	gag		595
Ser	Asn	Tyr	Asn	Asp	Pro	Gly	Ala	Asp	Ser	Asn	Ala	Val	Lys	Ile	Glu		
	150				155					160					165		
ttc	cag	goc	gat	tgc	tac	goc	ggc	att	tgg	gct	aat	cac	tac	agg	gaa		643
Leu	Gln	Ala	Asp	Cys	Tyr	Ala	Gly	Ile	Trp	Ala	Asn	His	Ser	Ser	Glu		
			170					175						180			
ggc	cgc	gat	cgc	cta	ctc	caa	cgc	atc	acc	gaa	tct	gag	cgc	gat	tcc		691
Gly	Pro	Asp	Pro	Leu	Leu	Gln	Pro	Ile	Thr	Glu	Ser	Glu	Leu	Asp	Ser		
			185					190					195				
gct	ctc	cgc	gct	gca	acc	goc	gtg	ggc	gac	gac	aat	atc	cag	caa	cga		739
Ala	Leu	Leu	Ala	Ala	Ser	Ala	Val	Gly	Asp	Asp	Asn	Ile	Gln	Gln	Arg		
		200					205					210					
tcc	ggt	goc	gat	gtc	aat	cct	gaa	agg	tgg	act	cac	ggc	tca	tgc	cag		787
Ser	Gly	Gly	Asp	Val	Asn	Pro	Glu	Ser	Trp	Thr	His	Gly	Ser	Ser	Gln		
	215					220					225						
caa	cgc	aaa	gac	goc	ttc	ctc	goc	ggc	tac	aac	acc	ggc	cag	atg	agg		835
Gln	Arg	Lys	Asp	Ala	Phe	Leu	Ala	Gly	Tyr	Asn	Thr	Gly	Gln	Met	Ser		
	23				235					240					245		

gac tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg 884  
 Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala  
 250 255

attttggaag tat 897

1210 - 16

1211 - 153

1212 - PRT

1213 - *Corynebacterium glutamicum*

1430 - 16

Leu Leu Leu Gly Gly Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly  
 1 5 10 15

Asp His Thr Gln Ile Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe  
 20 25 30

Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg  
 35 40 45

Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu  
 50 55 60

Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe  
 65 70 75 80

Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly  
 85 90 95

Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe  
 100 105 110

Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln  
 115 120 125

Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu  
 130 135 140

Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn  
 145 150 155 160

Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala  
 165 170 175

Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu  
 180 185 190

Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp  
 195 200 205

Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Gln Ser Trp Thr  
 210 215 220

His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn  
 225 230 235 240

Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn  
 245 250 255

Asp Ala

&lt;210&gt; 17

&lt;211&gt; /71

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;216&gt;

&lt;217&gt; CDS

&lt;222&gt; (101)..(743)

&lt;223&gt; EX01207

&lt;410&gt; 17

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				gtg agc aga atc tat	115	
				Val Ser Arg Ile Tyr		
				1 5		

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Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val	163					
10 15 20						

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25 30 35						

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Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu	269					
40 45 50						

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Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val	307					
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Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln	355					
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Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile	403					
90 95 100						

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ttcttgatc	tcaacggcag	agcgcgtttt	gttacagcgc	gtaaacctgtg	accttgaaaa	60
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly	451					
105 110 115						

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Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu	499					
120 125 130						

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Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His	547					
135 140 145						

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ttcttgatc	tcaacggcag	agcgcgtttt	gttacagcgc	gtaaacctgtg	accttgaaaa	60
Asn Cys Ala Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn	595					
150 155 160 165						

gtc ggt gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643  
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser  
170 175 180

acc atc gtg gat att tca ggc acc gca cca aag att ttg cgt gag ggt 691  
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly  
185 190 195

gcc atc agc gca gaa cgc gtc ggc gaa gta ctt gga gtg tgg gca gaa 739  
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu  
200 205 210

agc ctg agc taaatgggag taggttggc ggg 771  
Ser Leu Arg  
215

<210> 18

<211> 216

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 18

Val Ser Arg Ile Tyr Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly  
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Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu  
20 25 30

Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu  
35 40 45

Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro  
50 55 60

Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His  
65 70 75 80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly  
85 90 95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu  
100 105 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val  
115 120 125

Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala  
130 135 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Gln Ala Arg Gln  
145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala  
165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys  
180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu

195 200 205

Gly Val Ser Ala Glu Ser Leu Arg  
110 215

0010- 19  
0011- 1026  
0012- DNA  
0013- Corynebacterium glutamicum

0010-  
0011- CDS  
0012- (111)..(1003)  
0013- RX000657

01 01 19  
r ggggtagg ggtatccggg ct caacttag aggtgttaga gatcatgagt ttccacgaac 60

tctacggcag gattcaacaa tcatgaaag gtccaccgac atg agc act gaa gac 115  
Met Ser Thr Glu Asp  
1 5

att ctg gtc gta gca gta tat ggc tgg gac gcc tca aaa caa gct gtt 163  
Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val  
10 15 20

acc agc gct gca aat acc tcc aac aaa agt ggc att cca ctt cgc ttg 211  
Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu  
25 30 35

ggt tcc agc tcc acc atg cct cag ttc ctg tcc tca gag gga atg gtt 259  
Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val  
40 45 50

cca cca caa gag ctt ttc tat gac ctg cag gcc gaa gcc ctg gaa aag 307  
Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys  
55 60 65

att caa gaa gcc cgt gac atc gcc cat gag gta gcc cca gaa atc aag 355  
Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys  
70 75 80 85

atc ggg cac acc atc gct caa ggc agt ccc atc gac atg ctg ttg gaa 403  
Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu  
90 95 100

atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctg gcc 451  
Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly  
105 110 115

gga ctg tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc 499  
Gly Leu Ser Gly Met Val Met Ser Val Ser Gly Ala Val Val Ser  
120 125 130

caa cca aag tgt cca gtc att gtt gtc cgt gaa gac agc gca gtc aac 547  
His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn  
135 140 145

gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa 595  
Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu

150 155 160 165  
 gtc tcc caa cag gca acc gaa tac gca ttt gag gaa gct gaa gct cgt 643  
 Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg  
 170 175 180  
 gcc gcc gaa ctg gtt gca gtt cac acc tgg atg gac atg cag gta cag 691  
 Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln  
 185 190 195  
 gca cca ctc gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg 739  
 Ala Ser Leu Ala Gly Leu Ala Ala Glu Gln Gln Trp Asp Glu Val  
 200 205 210  
 gaa cgt cag caa acc gac atg ctg atc gaa gcc ctg gca cca ctg ctg 787  
 Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val  
 215 220 225  
 gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac gcc 835  
 Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg  
 230 235 240 245  
 cca gtt gcc gca ctt gca gaa gca tct gaa aac gag cag ctg cta ctg 883  
 Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val  
 250 255 260  
 ttc ggt tcc cat ggt cct gcc gga ttc aag gcc atg ctg ctt gcc tcc 931  
 Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser  
 265 270 275  
 acc acc gcc gca ctg ctg caa tcc gca ccc tgc cca atg atg gtc gtt 979  
 Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val  
 280 285 290  
 gcc cca cct gag aag att aag aag tagttttctt taagttttoga tgc 1026  
 Arg Pro Pro Glu Lys Ile Lys Lys  
 295 300

1210: 20

1211: 301

1212: PRT

1213: *Corynebacterium glutamicum*

1400: 20

Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala  
 1 5 10 15

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly  
 20 25 30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr  
 35 40 45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala  
 50 55 60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val  
 65 70 75 80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile





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cag	ctg	tgg	cag	cgt	gag	ctc	tgc	gag	tca	ctg	aat	ctt	cgt	ggc	cgc	211
Gln	Leu	Trp	Gln	Arg	Glu	Leu	Cys	Glu	Ser	Leu	Asn	Leu	Arg	Gly	Arg	
				25	30				35							
atc	ctg	atc	tcc	act	cac	gac	atc	aat	gga	acc	gtg	ggc	gga	gat	att	259
Ile	Leu	Ile	Ser	Thr	His	Gly	Ile	Asn	Gly	Thr	Val	Gly	Gly	Asp	Ile	
				40	45				50							
gat	gat	tgc	aag	ggg	tac	att	aaa	tac	acc	cgc	gag	tac	caa	ggc	ttc	307
Asp	Asp	Cys	Lys	Ala	Tyr	Ile	Lys	Lys	Thr	Arg	Glu	Tyr	Pro	Gly	Phe	
				55	60				65							
aac	cgc	atg	cag	ttt	agg	tgg	tcc	tgg	ggc	ggt	gag	gat	ttc	cca	cca	355
Asn	Arg	Met	Gln	Phe	Lys	Trp	Ser	Glu	Gly	Gly	Ala	Glu	Asp	Phe	Pro	
				70	80				85							
aag	ctc	agt	gtc	aaa	gtc	cac	gat	tac	atc	gtt	gac	ttc	ggc	ggt	cca	403
Lys	Leu	Ser	Val	Lys	Val	Arg	Asp	Glu	Ile	Val	Ala	Phe	Gly	Ala	Pro	
				90	95				100							
gat	gag	ctc	aaa	gtg	gtt	gaa	aac	ggc	ctc	gtc	ggc	ggc	ggc	gtt	cac	451
Asp	Glu	Leu	Lys	Val	Asp	Glu	Asn	Gly	Val	Val	Gly	Gly	Gly	Val	His	
				105	110				115				120			
ctg	aaa	cca	cag	cag	tcc	aat	gag	ttt	tgc	gaa	gac	cgt	ggc	gat	gaa	499
Leu	Lys	Pro	Gln	Gln	Val	Asn	Glu	Leu	Val	Glu	Ala	Arg	Gly	Asp	Glu	
				125	130				135							
gtt	gtg	tcc	ttt	gac	tcc	cac	aac	cca	atg	gaa	gac	cag	atc	ggc	aag	547
Val	Val	Phe	Phe	Asp	Gly	Arg	Asn	Ala	Met	Glu	Ala	Gln	Ile	Gly	Lys	
				135	140				145				150			
ttc	aag	gac	ggt	gtt	tcc	cac	gac	tta	aaa	acc	act	cac	gat	ttc	atc	595
Phe	Lys	Asp	Ala	Val	Val	Pro	Asp	Val	Glu	Thr	Thr	His	Asp	Phe	Ile	
				155	160				165				170			
gaa	gaa	att	gag	tct	tta	aaa	tac	gac	gat	ctc	aaa	gac	aac	ccc	gtg	643
Ala	Glu	Ile	Gln	Ser	Gly	Lys	Tyr	Asp	Asp	Leu	Lys	Asp	Lys	Pro	Val	
				175	180				185				190			
gtc	acc	tac	tgc	acc	gtc	gga	att	cgt	tgt	gag	atc	ctg	agt	tca	ctc	691
Val	Thr	Tyr	Cys	Thr	Gly	Gly	Ile	Arg	Cys	Glu	Ile	Leu	Ser	Ser	Leu	
				195	200				205				210			
atg	atc	aac	cgt	ggc	ttc	aaa	gag	gtc	tac	caa	atc	gat	ggc	ggc	atc	739
Met	Ile	Asn	Arg	Gly	Phe	Lys	Glu	Val	Tyr	Gln	Ile	Asp	Gly	Gly	Ile	
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gtt	cgc	tac	ggc	gag	cag	ttt	ggc	aac	aag	ggc	ctg	tgg	gaa	ggc	tcc	787
Val	Arg	Tyr	Gly	Glu	Gln	Phe	Gly	Asn	Lys	Gly	Leu	Trp	Glu	Gly	Ser	
				235	240				245				250			
ctc	tac	gtt	ttc	gat	tac	cgc	atg	cac	atg	gaa	ttc	ggc	gag	gat	tac	835
Leu	Tyr	Val	Phe	Asp	Lys	Arg	Met	His	Met	Glu	Phe	Gly	Glu	Asp	Tyr	
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aaa	gag	gtc	gga	cac	tac	atc	cac	tgc	gat	act	ccc	acc	aac	aaa	ttt	883
Lys	Glu	Val	Gly	His	Cys	Ile	His	Cys	Asp	Thr	Pro	Thr	Asn	Lys	Phe	

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc 931  
 Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys  
 265 270 275  
 ccg gat tgc ttc gcc aat gtt gag acc cgt cat tga aag cgc gaa cgc 979  
 Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg  
 280 285 290  
 tgt gca gcc att gct ggc gat ttc gct gag caa gga att gat cgc ctc 1027  
 Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu  
 295 300 305  
 gtt act tct taaaaagggt atgggtgggtg ggt 1059  
 Val Thr Ser  
 310

&lt;210&gt; 12

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 12

Val Ala Thr Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser  
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 Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu  
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 Asn Leu Asn Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr  
 35 40 45  
 Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg  
 50 55 60  
 Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly  
 65 70 75 80  
 Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val  
 85 90 95  
 Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val  
 100 105 110  
 Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu  
 115 120 125  
 Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu  
 130 135 140  
 Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr  
 145 150 155 160  
 Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu  
 165 170 175  
 Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu  
 180 185 190  
 Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln



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Glu	Ser	Leu	Gly	Ala	Glu	Ala	Gln	Ser	Phe	Pro	Gly	Ser	Gln	Ala	Gly	
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gtg	ctc	acc	acc	gag	ggc	gac	gga	aac	gca	ggc	att	gtt	gat	gac	act	461
Val	Leu	Thr	Thr	Glu	Arg	His	Gly	Asn	Ala	Arg	Ile	Val	Asp	Val	Thr	
			105					110						115		
cca	ggt	ggt	gtg	ggt	gaa	gca	ctc	gat	gag	ggc	aag	atc	tgc	att	ggt	469
Pro	Gly	Arg	Val	Arg	Glu	Ala	Leu	Asp	Glu	Gly	Lys	Ile	Cys	Ile	Val	
			120					125					130			
gct	ggt	ttc	cag	ggt	gtt	aat	aaa	gaa	acc	ggc	gat	gtc	acc	agg	tig	547
Ala	Gly	Phe	Gln	Gly	Val	Asn	Lys	Glu	Thr	Arg	Asp	Val	Thr	Thr	Leu	
			135					140					145			
ggt	ggt	ggt	ggt	ggt	tct	gac	acc	acc	gca	gtt	ggg	tig	gca	gat	ggt	545
Gly	Arg	Gly	Gly	Ser	Asp	Thr	Thr	Ala	Val	Ala	Leu	Ala	Ala	Ala	Leu	
			150					155				160			165	
aac	gct	gat	gtc	tgt	gag	att	tac	tgg	gac	gtt	gac	ggt	gtg	tat	acc	643
Asn	Ala	Asp	Val	Cys	Glu	Ile	Tyr	Ser	Asp	Val	Asp	Gly	Val	Tyr	Thr	
				170					175					180		
gct	gac	ggg	ggc	atc	gtt	gct	aac	gca	gag	aag	ctg	gaa	aag	ctc	agc	661
Ala	Asp	Pro	Arg	Ile	Val	Pro	Asn	Ala	Gln	Lys	Leu	Glu	Lys	Leu	Ser	
				185				190						195		
tta	gaa	gaa	atg	ctg	gaa	gct	gct	gtt	ggc	tac	aag	att	tig	gtg		769
Phe	Glu	Glu	Met	Leu	Glu	Leu	Ala	Ala	Val	Gly	Ser	Lys	Ile	Leu	Val	
			200					205					210			
ctg	ggc	ggt	gtt	gaa	tac	gct	ggt	gca	ttc	aac	gtc	cca	gtt	ccc	gtc	787
Leu	Arg	Ser	Val	Glu	Tyr	Ala	Arg	Ala	Phe	Asn	Val	Pro	Leu	Arg	Val	
			215					220								
ggc	tgg	tct	tat	agt	aac	gat	ccc	ggc	act	tig	att	goc	ggc	tct	atg	805
Arg	Ser	Ser	Tyr	Ser	Asn	Asp	Pro	Gly	Thr	Leu	Ile	Ala	Gly	Ser	Met	
						235						240			245	
gag	gat	att	gct	gtg	gaa	gaa	gca	gtc	gtt	acc	ggt	gtc	gca	acc	gat	883
Glu	Asp	Ile	Pro	Val	Glu	Glu	Ala	Val	Leu	Thr	Gly	Val	Ala	Thr	Asp	
						250						255			260	
aag	too	gaa	gac	aaa	gta	acc	gtt	ctg	ggt	att	tcc	gat	aag	cca	ggc	961
Lys	Ser	Glu	Ala	Lys	Val	Thr	Val	Leu	Gly	Ile	Ser	Asp	Lys	Pro	Gly	
					265				270					275		
gag	gct	ggg	aag	gtt	tta	ggt	ggg	tig	gct	gat	gca	gaa	atc	aac	att	979
Glu	Ala	Ala	Lys	Val	Phe	Arg	Ala	Leu	Ala	Asp	Ala	Glu	Ile	Asn	Ile	
			280					285					290			
gac	atg	gtt	ctg	cag	aac	gtc	tct	tct	gta	gaa	gac	ggc	acc	acc	gac	1027
Asp	Met	Val	Leu	Gln	Asn	Val	Ser	Ser	Val	Glu	Asp	Gly	Thr	Thr	Asp	
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atc	acc	tta	acc	tgc	gct	ggt	too	gac	ggc	ggc	ggc	ggg	atg	gag	atc	1075
Ile	Thr	Phe	Thr	Cys	Pro	Arg	Ser	Asp	Gly	Arg	Arg	Ala	Met	Glu	Ile	
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tig	aag	aag	ctt	cag	gtt	cag	ggc	aac	tgg	acc	aat	gtg	ctt	tac	gac	1123

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 cca ggt att acc gca gag ttc atg gaa gct ctg cgc gat gtc aac gtg 1219  
 Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val  
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 aac atc gaa ttg att tcc acc tct gag att cgt att tcc gtg ctg atc 1267  
 Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile  
 375 380 385  
 cgt gaa gct gat ctg gat gct gct gca cgt gca ttg cat gag cag ttc 1315  
 Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe  
 390 395 400 405  
 cag ctg tgc ggc ggc gaa gac gaa ggc gtc gtt cat gca ggc acc gga cgc 1363  
 Gln Leu Gly Gly Glu Asp Glu Ala Val Tyr Ala Gly Thr Gly Arg  
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&lt;110&gt; 24

&lt;111&gt; 421

&lt;112&gt; PRT

&lt;113&gt; Corynebacterium glutamicum

&lt;100&gt; 24

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 20 25 30  
 Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp  
 35 40 45  
 Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
 50 55 60  
 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
 65 70 75 80  
 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
 85 90 95  
 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
 100 105 110  
 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
 115 120 125  
 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg  
 130 135 140  
 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala  
 145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
 165 170 175  
 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
 180 185 190  
 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
 195 200 205  
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
 210 215 220  
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
 225 230 235 240  
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr  
 245 250 255  
 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
 260 265 270  
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
 275 280 285  
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 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg  
 305 310 315 320  
 Asn Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
 325 330 335  
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
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 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
 355 360 365  
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg  
 370 375 380  
 Leu Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
 385 390 395 400  
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 #111: 1155  
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 #114: QDS  
 #222: (101)..(1132)

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                                         Met Thr Thr Ile Ala
                                         1           5
gtt gtt ggt gca acc ggc cag gtc ggc cag gtt atg cgc acc ctt ttg 163
Val Val Gly Ala Thr Gly Gln Val Gly Gln Val Met Arg Thr Leu Leu
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Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg Phe Phe Ala Ser Pro
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cgt tcc gca ggc cgt aag att gaa ttc cgt ggc acg gaa atc gag gta 259
Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly Thr Glu Ile Glu Val
              40              45              50
gaa gac att act cag gca acc gag gag tcc ctc aag gac atc gac gtt 307
Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu Lys Asp Ile Asp Val
              55              60              65
cag ttc ttc tcc gct cga ggc acc gct tcc aag cag tcc gct cca ctg 355
Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys Glu Tyr Ala Pro Leu
              70              75              80              85
ttc gct gat gca ggc ggc act gtt gtc gat aac tct tct gct tgg cgc 403
Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn Ser Ser Ala Trp Arg
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cag gac gac gag gtt cca cca atc gtc tct gag gtc aac cct tcc gac 451
Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu Val Asn Pro Ser Asp
              105              110              115
cag gat tcc ctg gtc aag ggc att att gcg aac cct aac tgc acc acc 499
Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn Pro Asn Cys Thr Thr
              120              125              130
atg gct gcg atg cca gtg ctg aag cca ctt cac gat gca gct ggt ctt 547
Met Ala Ala Met Pro Val Leu Lys Pro Leu His Asp Ala Ala Gly Leu
              135              140              145
gta aag ctt cac gtt tcc tct tcc cag gct gtt tcc ggt tct ggt ctt 595
Val Lys Leu His Val Ser Ser Tyr Gln Ala Val Ser Gly Ser Gly Leu
              150              155              160              165
gca ggt gtg gaa acc ttg gca aag cag gtt gct gca gtt gga gac cac 643
Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala Ala Val Gly Asp His
              170              175              180
aac gtt gag ttc gtc cat gat gga cag gct gct gac gca ggc gat gtc 691
Asn Val Glu Phe Val His Asp Gly Gln Ala Ala Asp Ala Gly Asp Val
              185              190              195
gga cct tat gtt tca cca atc gct tac aac gtg ctg cca ttc gcc gga 739
Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val Leu Pro Phe Ala Gly
              200              205              210

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 cgc aac gaa ttc cgc aag att ctc ggt ctc cca gac ctc aag gtc tca 835  
 Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro Asp Leu Lys Val Ser  
 230 235 240 245  
 ggc acc tgc gtc cgc gtg cgc gtt ttc acc ggc cac acg ctg acc att 883  
 Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile  
 250 255 260  
 cac gcc gaa ttc gac aag gca atc acc gtg gac cag gcg cag gag atc 931  
 His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile  
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 Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu  
 280 285 290  
 gca gct gcc gcc att gac gaa ttc ctc gtt ggc cgc atc cgt cag gac 1027  
 Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp  
 295 300 305  
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 Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp  
 310 315 320 325  
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 Asn Leu Arg Lys Gly Ala Ala Leu Asn Phe Ile Gln Ile Ala Glu Leu  
 330 335 340  
 ctg gtt aag tcaaaacgc caattaaaaa ctc 1155  
 Leu Val Lys

8110-26

8111-344

8112-PRT

8113-Corynebacterium glutamicum

8100-26

Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Gln Val  
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 Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly  
 35 40 45  
 Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu  
 50 55 60  
 Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys  
 65 70 75 80  
 Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn  
 85 90 95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu  
 100 105 110  
 Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn  
 115 120 125  
 Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His  
 130 135 140  
 Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val  
 145 150 155 160  
 Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala  
 165 170 175  
 Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala  
 180 185 190  
 Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val  
 195 200 205  
 Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp  
 210 215 220  
 Glu Gln Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro  
 225 230 235 240  
 Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly  
 245 250 255  
 His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp  
 260 265 270  
 Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp  
 275 280 285  
 Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly  
 290 295 300  
 Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu  
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 <213> Corynebacterium glutamicum

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 <223> EXA02843

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 Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser  
 1 5 10  
 acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 153  
 Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp  
 15 20 25 30  
 cag tcc ggc ctg aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206  
 Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val  
 35 40 45  
 acc ggc aaa atc gtg aag aca act atc gac acc gac gca gcc acc acc 254  
 Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr  
 50 55 60  
 gac acc tac gat gca tgg ctg ggc ctt caa ctg ctg tcc caa cga gtt 302  
 Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val  
 65 70 75  
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 Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn  
 80 85 90  
 cat ctg gtg tgg acc aac ttc gga cgg tgc gca gtt gac ggt ttc gca 398  
 Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala  
 95 100 105 110  
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 Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser  
 115 120 125  
 gtc aac aag ttc cca ggc atg gtc gac tat gtg gtt ccc tgg ggc gtg 494  
 Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val  
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 145 150 155  
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 Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr  
 160 165 170  
 ttc ggc gct tcc atg gtt 605  
 Leu Gly Ala Ser Met Val  
 175 180

0010 28

0011 180

0012 PRT

0013 Corynebacterium glutamicum

0400 28

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly  
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Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser  
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Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg  
 35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr  
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Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg  
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Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val  
 85 90 95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr  
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Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile  
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Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr  
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Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly  
 165 170 175

Ala Ser Met Val  
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GENE 29  
 GEN1: 1231  
 GEN2: DNA  
 GEN3: Corynebacterium glutamicum

GENE  
 GEN1: CDS  
 GEN2: (101)..(1207)  
 GEN3: EXA12022

GENE 29  
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 Val Asn Ser Glu Leu  
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aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt 163  
 Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg  
 10 15 20

tig gta gat ata cgg agt cgg tcc ggt cag gaa aag cag att gct gat 211  
 Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp  
 25 30 35

gaa att gaa gat gcc ctt cgg aac ctt aat cta cct ggt gta gag gtc 259  
 Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val  
 40 45 50

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Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala	
55 60 65	
tgc agg gtc atg ctt gct ggt cat atc gat aca gtg ccg atc gag gac	355
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp	
70 75 80 85	
aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt gcc aac	403
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr	
90 95 100	
gtc gat atg aaa tct ggg ttg gag gtc tat ttg cat act ttt gcc aac	451
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr	
105 110 115	
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Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr	
120 125 130	
gag tgc gag gaa gtt gct gat aac ctc aat ggt ttg gcc cac att cgc	547
Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg	
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Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu	
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ctt act ggc ggc tgg att aag gag ggc tgg aag ggc aat ctg cgc atc	643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln Gly Asn Leu Arg Ile	
170 175 180	
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Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu	
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Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala	
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ggc tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa	787
Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu	
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Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile	
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cca gag ctg gag tgg atg aac ctc aac ttc cgt ttc gag ccg aat cgc	883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg	
250 255 260	
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Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp	
265 270 275	
ggt caa gag ggc atc gaa tgg gcc gta gaa gac ggg gcc ggc ggt gcc	979
Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala	
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Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val  
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 Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg  
 310 315 320 325  
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 345 350 355  
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 Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr  
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 Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr  
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 Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met  
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 Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu  
 100 105 110  
 His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu  
 115 120 125  
 Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly  
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 145 150 155 160  
 Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln  
 165 170 175

Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser  
 180 185 190  
 Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile  
 195 200 205  
 Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly  
 210 215 220  
 Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val  
 225 230 235 240  
 Ala Asn Asn Val Ile Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg  
 245 250 255  
 Phe Ala Pro Asn Arg Asp Leu Asn Glu Ala Ile Glu His Val Val Glu  
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 Thr Leu Glu Leu Asp Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp  
 275 280 285  
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 305 310 315 320  
 Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe  
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Gln

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 <113> EXA00044

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ttctcaccac cactcgttcc ctcaaccac aaggagcaac atg gct tcc gca act 115  
 Met Ala Ser Ala Thr  
 1 5

ttc acc ggc gtg atc cca ccc gta atg acc cca ctc cac gcc gac ggc 163  
 Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro Leu His Ala Asp Gly  
 10 15 20

agt	gtg	gat	gta	gaa	agc	ctc	ggc	aag	ctc	gtt	gac	cac	ctc	atc	aat	211
Ser	Val	Asp	Val	Glu	Ser	Leu	Arg	Lys	Leu	Val	Asp	His	Leu	Ile	Asn	
			25					30					35			
ggg	ggc	gtc	gac	gga	ctt	ttc	gca	ctg	ggc	tcg	tca	ggc	gaa	gca	gca	259
Gly	Gly	Val	Asp	Gly	Leu	Phe	Ala	Leu	Gly	Ser	Ser	Gly	Glu	Ala	Ala	
		40					45					50				
ttc	ctc	acc	ggc	gac	cag	ggc	aaa	ctc	gca	ctg	acc	acc	atc	atc	gag	307
Phe	Leu	Thr	Arg	Ala	Gln	Arg	Lys	Leu	Ala	Leu	Thr	Thr	Ile	Ile	Glu	
	55					60					65					
cac	acc	gca	ggc	ggc	ggc	gtt	ccc	gta	act	gct	ggg	gtc	att	gaa	acc	355
His	Thr	Ala	Gly	Arg	Val	Pro	Val	Thr	Ala	Gly	Val	Ile	Glu	Thr	Thr	
	70				75					80					85	
act	gct	ggc	gtg	att	gag	ctc	gtg	gaa	gat	ggc	ctg	gag	gct	ggc	ggc	403
Thr	Ala	Arg	Val	Ile	Glu	Leu	Val	Glu	Asp	Ala	Leu	Glu	Ala	Gly	Ala	
			9					95						100		
gaa	ggc	ctc	gtt	gac	act	gca	cat	ttc	tac	acc	ggc	acc	cac	gat	gtg	451
Glu	Gly	Leu	Val	Ala	Thr	Ala	Pro	Phe	Tyr	Thr	Arg	Thr	His	Asp	Val	
			105					110					115			
gaa	att	gaa	gaa	cac	ttc	ggc	aag	atc	cac	ggc	ggc	gct	cca	gat	att	499
Glu	Ile	Glu	Glu	His	Phe	Arg	Lys	Ile	His	Ala	Ala	Ala	Pro	Gln	Leu	
		120					125					130				
cca	ctg	ctt	ggc	tac	aac	atc	cca	gtg	tcg	gtg	cac	tcg	aac	ctc	aac	547
Pro	Leu	Phe	Ala	Tyr	Asn	Ile	Pro	Val	Ser	Val	His	Ser	Asn	Leu	Asn	
	135					140					145					
cca	gtc	atg	ctt	ttc	aag	ctc	gac	aag	gat	ggc	gtt	ctt	gca	ggc	acc	595
Pro	Val	Met	Leu	Leu	Thr	Leu	Ala	Lys	Asp	Gly	Val	Leu	Ala	Gly	Thr	
	150					155				160				165		
aag	gat	ccc	agt	ggc	aat	gat	gtc	gca	atc	ggc	tca	ctg	atc	gat	gct	643
Lys	Asp	Ser	Ser	Gly	Asn	Asp	Gly	Ala	Ile	Arg	Ser	Leu	Ile	Gln	Ala	
				170					175					180		
agt	gat	gat	ggt	gga	ctc	act	gag	cag	ttc	aaq	atc	ctc	acc	ggc	agg	691
Arg	Asp	Asp	Ala	Gly	Leu	Thr	Gln	Gln	Phe	Lys	Ile	Leu	Thr	Gly	Ser	
			185					190					195			
gaa	acc	acc	gtt	gat	ttc	ggc	tac	ctt	ggc	ggc	ggc	gat	gga	gtt	gtc	739
Glu	Thr	Thr	Val	Asp	Phe	Ala	Tyr	Leu	Ala	Gly	Ala	Asp	Gly	Val	Val	
		200				205						210				
cca	ggc	ctg	ggc	aat	gtt	gat	cat	gca	gca	tac	gca	gct	tta	gca	aaa	787
Pro	Gly	Leu	Gly	Asn	Val	Asp	Pro	Ala	Ala	Tyr	Ala	Ala	Leu	Ala	Lys	
	215					220					225					
ctc	tgc	ctc	gat	gga	aag	tgg	gca	gaa	gct	gct	gct	ttg	cag	aaq	ggc	835
Leu	Cys	Leu	Asp	Gly	Lys	Trp	Ala	Glu	Ala	Ala	Ala	Leu	Gln	Lys	Arg	
	230				235					240				245		
atc	aac	cac	ctc	ttc	cac	atc	gtc	ttc	gtg	gga	gac	acc	tcg	cat	atg	883
Ile	Asn	His	Leu	Phe	His	Ile	Val	Phe	Val	Gly	Asp	Thr	Ser	His	Met	
			250					255					260			
ccc	gga	ccc	agg	gct	ggc	ttg	ggc	ggc	ttc	aaq	aca	gca	ctc	gca	cac	931



Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His  
265 270 275

ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc 979  
Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu  
280 285 290

agc gac gaa gaa act gct ggc att cac gcc att gtt gat gaa ttc ctg 1027  
Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu  
295 300 305

tac acc gct taaggccac acctcatgac tga 1059  
Tyr Thr Ala  
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<L10> 12

<L11> 112

<L12> 8RT

<L13> Corynebacterium glutamicum

<400> 12

Met Ala Ser Ala Thr Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro  
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Leu His Ala Asp Gly Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val  
20 25 30

Arg His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser  
35 40 45

Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Glu Arg Lys Leu Ala Leu  
50 55 60

Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly  
65 70 75 80

Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala  
85 90 95

Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr  
100 105 110

Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala  
115 120 125

Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val  
130 135 140

His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly  
145 150 155 160

Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg  
165 170 175

Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys  
180 185 190

Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly  
195 200 205

Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr  
210 215 220

Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala  
225 230 235 240

Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly  
245 250 255

Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys  
260 265 270

Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val  
275 280 285

Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile  
290 295 300

Val Asp Glu Phe Leu Tyr Thr Ala  
305 310

<210> 33

<211> 167

<212> CNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101).. 844)

<223> EXA00863

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gtttcaaaaa ctcttcgccc caacgaaatg aaggagcata atg gga atc aag gtt 115  
Met Gly Ile Lys Val  
1 5

ggc gtt ctc gga gcc aaa ggc cgt gtt ggt caa act att gtg gca gca 163  
Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala  
10 15 20

gtc aat gag tcc gac gat ctg gag ctt gtt gca gag atc ggc gtc gac 211  
Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp  
25 30 35

gat gat ttg agc ctt ctg gta gac aac ggc gct gaa gtt gtc gtt gac 259  
Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp  
40 45 50

ttc aac act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac 307  
Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn  
55 60 65

aac ggc att tct gcg gtt gtt gga acc acg ggc ttc gat gat gct cgt 355  
Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg  
70 75 80 85

ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt 403  
Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val

90	95	100	
ctg atc gca cct aac ttt gct atc tct ggc gtg ttg acc atg gtc ttt			451
Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val Leu Thr Met Val Phe			
105	110	115	
too aag cag gct gcc cgc ttc ttc gaa tca gct gaa gtt att gag ctg			499
Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala Glu Val Ile Glu Leu			
120	125	130	
cac cac ccc aac aag ctg gat gca cct tca ggc acc ggc atc cac act			547
His His Pro Asn Lys Leu Asp Ala Pro Ser Gly Thr Ala Ile His Thr			
135	140	145	
gct caa ggc att gct ggc gca cgc aaa gaa gca ggc atg gac gca cag			595
Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala Gly Met Asp Ala Gln			
151	155	160	165
cca caa ggc acc gag cag gca cct gag ggt too cgt ggc gca agc gta			643
Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser Arg Gly Ala Ser Val			
170	175	180	
gat cga atc cgc gtt cat gca gtc cgc atg too ggc atg gtt gct cac			691
Asp Gly Ile Pro Val His Ala Val Arg Met Ser Gly Met Val Ala His			
185	190	195	
gag caa gtt atc ttt ggc acc cag ggt cag acc ttg acc atc aag cag			739
Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr Leu Thr Ile Lys Gln			
200	205	210	
gac tca tat gat cgc aac tca ttc gca cca ggt gtc ttc gtc ggt ggc			787
Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly Val Leu Val Gly Val			
215	220	225	
gga caa att gca cag cac cca ggc cta gtc gta gga ctt gag cat cac			835
Arg Asn Ile Ala Gln His Pro Gly Leu Val Val Gly Leu Glu His Tyr			
231	235	240	245
ata cgc ctg taacaggctca ttccagcagc ggc			867
Leu Gly Leu			

0110 - 34

0111 - 248

0112 - PRT

0113 - Corynebacterium glutamicum

0400 - 34

Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln  
 1 5 10 15

Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala  
 20 25 30

Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala  
 35 40 45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu  
 50 55 60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly  
 65 70 75 80  
 Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys  
 85 90 95  
 Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val  
 100 105 110  
 Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala  
 115 120 125  
 Gln Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly  
 130 135 140  
 Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala  
 145 150 155 160  
 Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser  
 165 170 175  
 Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser  
 180 185 190  
 Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr  
 195 200 205  
 Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly  
 210 215 220  
 Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val  
 225 230 235 240  
 Gly Leu Glu His Tyr Leu Gly Leu  
 245

GI01: 35  
 GI11: 373  
 GI12: DNA  
 GI13: *Corynebacterium glutamicum*

GI14:  
 GI15: CDS  
 GI16: (101)..(150)  
 GI17: EXA00364

GI00: 35  
 acagacacca ggctagctcg taggaacttga gcattacctt ggctgtataa ggctcatttc 60  
 accaggggggt ggaatttttt aaaaggagagc tttaaagggt gtg gcc gaa caa gtt 115  
 Val Ala Glu Gln Val  
 1 5  
 aaa ttg agc gtg gag ttg ata ggc tgc agt tct ttt act cca ccc gct 163  
 Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala  
 10 15 20  
 gat gtt gag tgg tca act gat gtt gag ggc ggc gaa gca ctg gtc gag 211  
 Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu  
 25 30 35

ttt ggg ggt cgt gcc tgc tac gaa act ttt gat aag ccg aac cct cga 259  
 Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg  
 40 45 50

act gct tcc aat gct ggg tat ctg cgc cac atc atg gaa gtg ggg cac 307  
 Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His  
 55 60 65

act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att 315  
 Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile  
 70 75 80 85

tct cgg tcc ggg acc cat gta ttg gtc cga cac ctc cat ttt tcc ttc 403  
 Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe  
 90 95 100

tct caa ttg tct cag cgt ttc gtg cac agc gga gta ttg gaa gta gtg 451  
 Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val  
 105 110 115

gtg ccc act ctg atc gat gta gat ccg cag ttg ctt gaa ctt ttc atg 499  
 Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met  
 120 125 130

ccc gcc atg gat gag tct cag ttc gct ttc aat gag ctg ctt aat ggg 547  
 His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala  
 135 140 145

ttg gaa gaa aaa ctt ggc gat gaa ccg aat gaa ctt tta agg aaa aag 595  
 Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Cys Lys  
 150 155 160 165

caa gct cgt caa gca gct cgc gct gtg ctg ttc aac gct aca gag tcc 643  
 Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser  
 170 175 180

aga atc gtg gtg tct gga aac ttc cgc acc tgg aag cat ttc att ggc 691  
 Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly  
 185 190 195

atg cga gcc apt gaa cat gaa gac gtc gaa atc cgc gaa gta ggc gta 739  
 Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val  
 200 205 210

gaa tgt tta aga aag ctg ccg gta gca ggc cca act gtt ttc ggt gat 787  
 Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp  
 215 220 225

ttt gag att gaa act ttg gca gac gga ttg caa atg gca aca agc ccg 835  
 Phe Gln Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro  
 230 235 240 245

tat gtc atg gac ttt taacgcaaaag ctcacaccca cga 873  
 Tyr Val Met Asp Phe  
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<210> 16  
 <211> 250  
 <212> PRT

<213> Corynebacterium glutamicum

<100> 36

Val Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser  
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Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala  
20 25 30

Ile Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp  
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile  
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met  
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His  
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly  
100 105 110

Ile Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu  
115 120 125

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn  
130 135 140

Ile Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala  
145 150 155 160

Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro  
165 170 175

Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp  
180 185 190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile  
195 200 205

Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro  
210 215 220

Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln  
225 230 235 240

Met Ala Thr Ser Pro Tyr Val Met Asp Phe  
245 250

<100> 37

<110> 408

<120> DNA

<130> Corynebacterium glutamicum

<220>

<221> CDS

<222> (69)..(608)

<223> EXA02843

4400-37

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tggaagtc atg aat aat gct tcc gca acc gga att gca aca ctg acc tcc 110  
 Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser  
 1 5 10

acc ggc gac gtc ctg gac gtc tgg tat cca gaa atc ggg tcc acc gac 150  
 Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp  
 15 20 25 30

cag tcc gag ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 200  
 Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val  
 35 40 45

ccc cgc aaa atc gtc aag aca aat atc gac acc gac gca gcc ccc acc 250  
 Thr Arg Lys Ile Val Phe Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr  
 50 55 60

ccc acc ttc gat gca tgg ctg cgc ctt cca cta cta tcc cca cgc gtt 300  
 Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val  
 65 70 75

ccc ggc cct cca acc atc aac cta gac ggc att ttc ggc cta cta aac 350  
 Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn  
 80 85 90

cct ttc gtc tgg acc aac ttc gga cgc tgc gca gtt gac ggt ttc gca 400  
 Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala  
 95 100 105 110

atc acc cgc gag cgc ctg tca cgc cga ggc caa gtt aag gtt tat agc 450  
 Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser  
 115 120 125

gtc gac aag ttc cca cgc atg gtc gac tat gtc gtt ccc tcc ggc gtc 500  
 Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val  
 130 135 140

gpc atc ggt gac gcc gac cgc gtc cga ctt ggc ggc tac ctg gca gat 550  
 Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp  
 145 150 155

gpc acc acc gtc atg cat gag ggc ttc gtc aac ttc aac gct ggc aag 600  
 Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr  
 160 165 170

ctc gcc gct tcc atg gtt 608  
 Leu Gly Ala Ser Met Val  
 175 180

4210-38

4211-120

4212-PRT

4213-Corynebacterium glutamicum

4400-38

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly  
 1 5 10 15

Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser  
                   20                  25                  30  
 Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg  
                   35                  40                  45  
 Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr  
                   50                  55                  60  
 Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg  
                   65                  70                  75                  80  
 Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val  
                   85                  90                  95  
 Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr  
                  100                 105                 110  
 Asp Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp  
                  115                 120                 125  
 Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile  
                  130                 135                 140  
 Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr  
                  145                 150                 155                 160  
 Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly  
                  165                 170                 175  
 Ala Ser Met Val  
                  180

0110-19  
 0111-1143  
 0112-DNA  
 0113-Corynebacterium glutamicum

0110-  
 0111-CD8  
 0112-(101)..(1120)  
 0113-RXN00358

0400-19  
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 ggtcctgatg aaagagatgt cccatgaatca tcatcctaagt atg cat ctc ggt aag 115  
   Met His Leu Gly Lys  
   1                  5  
 ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163  
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met  
                   10                  15                  20  
 acc aac atc cgc gta gct atc gtc gcc tac gga aac ctg gga cgc agc 211  
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser  
                   25                  30                  35  
 gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259



Val	Glu	Lys	Leu	Ile	Ala	Lys	Gln	Pro	Asp	Met	Asp	Leu	Val	Gly	Ile		
		40					45					50					
ttc	tgc	cac	cgg	gac	acc	ctc	gac	aca	aag	aag	cca	gtc	ttt	gat	gtc	397	
Phe	Ser	Arg	Arg	Ala	Thr	Leu	Asp	Thr	Lys	Thr	Pro	Val	Phe	Asp	Val		
	55					60					65						
gac	gac	gtg	gac	aag	cac	gac	gac	gtg	gac	gtg	ctg	tcc	ctg	tgg		395	
Ala	Asp	Val	Asp	Lys	His	Ala	Asp	Asp	Val	Asp	Val	Leu	Phe	Leu	Cys		
	70				75					80					85		
atg	ggc	tac	gac	acc	gac	atc	cct	gag	cag	gca	cca	aag	tcc	gac	cac	403	
Met	Gly	Ser	Ala	Thr	Asp	Ile	Pro	Glu	Gln	Ala	Pro	Lys	Phe	Ala	Gln		
				90				95					100				
tcc	gac	tac	acc	gta	gac	acc	cac	gac	aac	cac	cgc	gac	atc	cca	cgc	461	
Phe	Ala	Cys	Thr	Val	Asp	Thr	Tyr	Asp	Asn	His	Arg	Asp	Ile	Pro	Arg		
			105					110					115				
cac	cgc	cag	gtc	atg	aac	gaa	gac	gac	acc	gca	gac	ggc	aac	gtt	gca	499	
His	Arg	Gln	Val	Met	Asn	Glu	Ala	Ala	Thr	Ala	Ala	Gly	Asn	Val	Ala		
	120					125						130					
ctg	gtc	cct	acc	ggc	tgg	gat	cca	gga	atg	tcc	tcc	atc	aac	cgc	gtc	547	
Leu	Val	Ser	Thr	Gly	Trp	Asp	Pro	Gly	Met	Phe	Ser	Ile	Asn	Arg	Val		
	135					140					145						
cac	gca	gag	gca	gtc	tta	gac	gag	cac	cag	cag	cac	acc	tcc	tgg	ggc	595	
Tyr	Ala	Ala	Ala	Val	Leu	Ala	Glu	His	Gln	Gln	His	Thr	Phe	Trp	Gly		
	150				155				160					165			
cca	ggt	cgg	cca	cag	ggc	cac	cca	gat	gct	tgg	cga	cgc	atc	cct	ggc	643	
Pro	Gly	Leu	Ser	Gln	Gly	His	Ser	Asp	Ala	Leu	Arg	Arg	Ile	Pro	Gly		
			170					175					180				
gtt	caa	aag	gca	gtc	cag	cac	acc	ctc	cca	tcc	gaa	gac	gac	ctc	gaa	691	
Val	Gln	Lys	Ala	Val	Gln	Tyr	Thr	Leu	Pro	Ser	Glu	Asp	Ala	Leu	Glu		
		185						190					195				
aag	gac	cgc	cgc	ggc	gaa	gac	ggc	gac	ctt	acc	gga	aag	caa	acc	cac	739	
Lys	Ala	Arg	Arg	Gly	Glu	Ala	Gly	Asp	Leu	Thr	Gly	Lys	Gln	Thr	His		
	200						205					210					
aag	cgc	caa	tgc	tcc	gtg	gtt	gac	gac	ggc	gac	gat	cac	gag	cgc	atc	787	
Lys	Arg	Gln	Cys	Phe	Val	Val	Ala	Asp	Ala	Ala	Asp	His	Glu	Arg	Ile		
	215					220					225						
gaa	aac	gac	atc	cgc	acc	atg	cct	gat	cac	tcc	gtt	ggc	tac	gaa	gtc	835	
Glu	Asn	Asp	Ile	Arg	Thr	Met	Pro	Asp	Tyr	Phe	Val	Gly	Tyr	Glu	Val		
	230				235					240				245			
gaa	gtc	aac	tcc	atc	gac	gaa	gca	acc	tcc	gac	tcc	gag	cac	acc	ggc	883	
Glu	Val	Asn	Phe	Ile	Asp	Glu	Ala	Thr	Phe	Asp	Ser	Glu	His	Thr	Gly		
		250						255				260					
atg	cca	cac	ggt	ggc	cac	gtg	att	acc	acc	ggc	gac	acc	ggt	ggc	tcc	931	
Met	Pro	His	Gly	Gly	His	Val	Ile	Thr	Thr	Gly	Asp	Thr	Gly	Gly	Phe		
		265						270				275					
aac	cac	acc	gtg	caa	tac	atc	ctc	aag	ctg	gac	cga	aac	cca	gat	tcc	979	
Asn	His	Thr	Val	Glu	Tyr	Ile	Leu	Lys	Leu	Asp	Arg	Asn	Pro	Asp	Phe		

280 285 290  
acc got too tca cag atc got ttc ggt cgc gca got cac cgc atg aag 1027  
Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys  
295 300 305  
cag cag ggc caa agc gga got ttc acc gtc ctc gaa gtt got cca tac 1075  
Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr  
310 315 320 325  
ctg ctc too cca gag aac ttg gac gat ctg atc gca cgc gac gtc 1120  
Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val  
330 335 340  
taatttagot cagaggggcaa gga 1143

&lt;210&gt; 40

&lt;211&gt; 140

&lt;212&gt; BRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 40

Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu  
1 5 10 15  
Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly  
20 25 30  
Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met  
35 40 45  
Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr  
50 55 60  
Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp  
65 70 75 80  
Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala  
85 90 95  
Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His  
100 105 110  
Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala  
115 120 125  
Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe  
130 135 140  
Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln  
145 150 155 160  
His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu  
165 170 175  
Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser  
180 185 190  
Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr  
195 200 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala  
 210 215 220  
 Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe  
 225 230 235 240  
 Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp  
 245 250 255  
 Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly  
 260 265 270  
 Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp  
 275 280 285  
 Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala  
 290 295 300  
 Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu  
 305 310 315 320  
 Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile  
 325 330 335  
 Ala Arg Asp Val  
 340

0210 - 41  
 0211 - 953  
 0212 - DNA  
 0213 - Corynebacterium glutamicum

0214 -  
 0215 - CDS  
 0216 - (101)..(953)  
 0217 - PRXA10382

0400 - 41  
 aatagatcag cgcacccgtg gtggaaccaa aagggtcaac aatacgaaac gttcgttttc 50  
 ggtcttgcgtg aaagagatgt ccctgaatca tcatctaaat atg cat ctc ggt aag 115  
 Met His Leu Gly Lys  
 1 3  
 ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163  
 Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met  
 11 15 20  
 gcc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211  
 Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser  
 25 30 35  
 gtc aac aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259  
 Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile  
 40 45 50  
 ttc tgc cgc cgg gcc acc ctc gac aca aag aag cca gtc ttt gat gtc 307  
 Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val  
 55 60 65

gac gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc	355
Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys	
70 75 85	
atg gcc tcc gcc acc gac atc cct gag cag gcc cca aag ttc gcc cag	403
Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln	
90 95 100	
ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc	451
Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg	
105 110 115	
cac gcc cag gtc atg aac gaa gcc gcc acc gcc gcc gcc aac gtt gca	499
His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala	
120 125 130	
ctg ttc tct acc gcc tgg gat cca gga atg ttc tcc atc aac gcc gtc	547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val	
135 140 145	
cat cca gag gca gtc tta gcc gag cac cag cag cac acc ttc tgg gcc	595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly	
150 155 160 165	
cca agt ttg tca cag gcc cac tcc gat gct ttg cga cgc atc cct gcc	643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly	
170 175 180	
gtt caa aag gca gtc cag tac acc cct cca tcc gaa gac gcc ctg gaa	691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu	
185 190 195	
aag gcc gcc gcc gcc gaa gcc gcc gcc gat att acc gcc aag caa acc cac	739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His	
200 205 210	
aag gcc caa tgc ttc gtg gtt gcc gag gag gcc gat cac gag gcc atc	787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile	
215 220 225	
gaa aac gac atc gcc acc atg cct gat tac ttc gtt gcc tac gaa gtc	835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val	
230 235 240 245	
gaa ttc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc gcc	883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly	
250 255 260	
atg cca cac ggt gcc cac gtg att acc acc gcc gac acc ggt gcc ttc	931
Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe	
265 270 275	
aac cac acc gtg gaa tac atc ctc aag	958
Asn His Thr Val Glu Tyr Ile Leu Lys	
280 285	

<210 - 42  
 <211 - 286  
 <212 - PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 42

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Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
 1          5          10          15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
 20          25          30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
 35          40          45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
 50          55          60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
 65          70          75

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
 80          85          90

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
 95          100          105

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
 110          115          120

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
 125          130          135

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
 140          145          150

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
 155          160          165

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
 170          175          180

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
 185          190          195

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
 200          205          210

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
 215          220          225

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
 230          235          240

Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
 245          250          255

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys
 260          265          270
 275          280          285

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&lt;410&gt; 43

&lt;211&gt; 1400

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;210&gt;

&lt;211&gt; CDS

&lt;212&gt; (1)..(1377)

&lt;213&gt; EXA90972

&lt;100&gt; 43

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ccg gca cct ggt tgg cgt ttc cgc acc gga gaa gat gta aca atg gct 48
Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala
      1           3           10           15

aac gtt gaa aat ttc aat gaa cct ccc gca cac gta tgg cca cgc aat 96
Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
      20           25           30

gct gtg cgc cca gaa gac ggc gtt gtc acc gtc gct agt gtg cct ctg 144
Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
      35           40           45

cct gac ctg gat gaa gaa tac gga acc cca ctg ttc gta gtc cac gag 192
Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
      50           55           60

gag gat ttc cat tcc cgc cct cga gac atg gct acc gca ttc cgt gga 240
Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
      65           70           75           80

ccc cgc aat gta cac tac gaa cct aaa gag ttc ctg acc aag acc att 288
Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
      85           90           95

gca cgt tgg gtt gat gaa gag ggt ctg gca ctg gac att gaa tcc atc 336
Ala Arg Trp Val Asp Gln Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
      100           105           110           115

aac gaa ctg ggt att gcc ctg gca gct ggt ttc cca acc agc cgt atc 384
Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
      120           125

acc gag cac ggt aac aac aaa ggc gta gag ttc ctg cgc gag ttg gtt 432
Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
      130           135           140

caa aac ggt gtt gga cac gtc gtt ctg gac tcc gca cag gaa cta gaa 480
Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
      145           150           155           160

ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg 528
Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
      165           170           175

atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc 576
Ile Arg Val Lys Pro Gly Ile Gln Ala His Thr His Glu Phe Ile Ala
      180           185           190

act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc 624
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
      195           200           205

gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg 672

```

Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu 210 215 220	
gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc Val Gly Leu His Cys His Val Gly Ser Glu Val Phe Asp Ala Glu Gly 225 230 235 240	730
ttc aag ctg gca gaa gaa ggc gtc ttc ggc ctg tac tca cag atc cac Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Glu Ile His 245 250 255	765
agt gaa ctg ggc gtt gcc att cct gaa ctg gat ctg ggt ggc gga tac Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr 260 265 270	810
ggc att gcc tat acc gca gct gaa gaa cca ctg aac gtc gaa gaa gtc Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val 275 280 285	864
gcc tcc gac ctg ctg acc gca gtc gga aaa atg gaa ggc gaa cta ggc Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly 290 295 300	912
atc gac gca cca acc gtc att gtt gag cct ggc cgc gct atc gca ggc Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly 305 310 315 320	960
gcc tcc acc gtc acc atc tac gaa ttc ggc acc acc aaa gac ttc cac Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His 325 330 335	1008
gtc gac gac gac aaa acc ggc gtt tac atc gcc gtc gac gga ggc atc Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met 340 345 350	1056
tcc gac aac atc ggc cca gca ctg tac ggc tcc gaa tac gac gcc ggc Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg 355 360 365	1104
gtc gta tcc ccc ttc gcc gaa gga gac cca gta agc acc ggc atc gtc Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val 370 375 380	1152
ggc tcc cac tcc gaa tcc ggc gat atc ctg atc aac gat gaa atc tac Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr 385 390 395 400	1200
ccn tat gac atc acc agc ggc gac ttc ctt gca ctg gca gcc acc ggc Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly 405 410 415	1248
gca tac tgc tac gcc atg agc tcc ggc tac aac gcc ttc aca ggc ccc Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro 420 425 430	1296
acc gtc gtc tcc gtc cgc gct ggc agc tcc ggc ctg atg ctg cgc cgc Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg 435 440 445	1344
gaa acg ctg gac gac atc ctg tca cta gag gca taacgctttt cgaagcctga Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala	1397

450

455

622

1400

1210 - 44

1211 - 459

1212 - PRT

1213 - *Corynebacterium glutamicum*

1400 - 44

Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala  
 1 5 10 15

Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn  
 20 25 30

Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu  
 35 40 45

Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu  
 50 55 60

Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly  
 65 70 75 80

Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile  
 85 90 95

Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile  
 100 105 110

Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile  
 115 120 125

Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val  
 130 135 140

Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu  
 145 150 155 160

Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu  
 165 170 175

Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala  
 180 185 190

Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser  
 195 200 205

Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu  
 210 215 220

Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly  
 225 230 235 240

Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His  
 245 250 255

Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr  
 260 265 270



Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val  
 275 280 285  
 Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly  
 290 295 300  
 Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly  
 305 310 315 320  
 Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His  
 325 330 335  
 Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met  
 340 345 350  
 Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg  
 355 360 365  
 Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val  
 370 375 380  
 Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr  
 385 390 395 400  
 Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly  
 405 410 415  
 Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro  
 420 425 430  
 Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg  
 435 440 445  
 Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala  
 450 455

#110: 45  
 #111: 2121  
 #112: DNA  
 #113: Corynebacterium glutamicum

#120:  
 #121: CDS  
 #122: (101)..(2093)  
 #123: EXA12653

#400: 45  
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 aacgggoggtt ttcattccaa taacccgcac agggaaaacta atg ata ccg aag ccc 115  
 Met Ile Pro Lys Pro  
 1 3  
 gag atg acc gac tta tat tta gag gac ctg tta aat gag ggt tgg gaa 163  
 Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu  
 10 15 20  
 aag att cgg tcc gcc aag gat att tcc gaa ctt agg aca gtt cta aaa 211  
 Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys

25						30						35						
gag	gtt	tcc	tcc	caa	att	cag	gaa	cga	gct	ggg	aaa	aaa	gat	gaa	gaa	259		
Glu	Val	Ser	Ser	Gln	Ile	Gln	Glu	Arg	Ala	Gly	Lys	Lys	Asp	Glu	Glu			
40						45						50						
egg	gga	atg	ggg	goc	act	tgg	egg	gag	ctg	tac	ccc	agg	atc	gtg	gaa	307		
Trp	Gly	Met	Gly	Ala	Thr	Trp	Arg	Glu	Leu	Tyr	Pro	Ser	Ile	Val	Glu			
55						60						65						
cgg	gct	tcc	tac	gaa	ggg	cgt	gac	agg	cta	atc	gga	ttt	gat	cac	tta	355		
Arg	Ala	Ser	Tyr	Glu	Gly	Arg	Asp	Ser	Leu	Ile	Gly	Phe	Asp	His	Leu			
70						75						80						85
goc	egg	gaa	atg	gaa	aga	tta	goc	ttc	ggc	cca	cca	tcc	gaa	agt	ttt	403		
Ala	Arg	Glu	Met	Glu	Arg	Leu	Ala	Phe	Gly	Pro	Pro	Ser	Glu	Ser	Phe			
90						95						100						
gaa	tac	ctc	caa	gaa	ctc	gta	caa	tcc	aga	gtg	gta	gac	atc	act	cac	451		
Glu	Tyr	Leu	Gln	Glu	Leu	Val	Lys	Ser	Gly	Val	Val	Asp	Ile	Thr	His			
105						110						115						
ctg	cat	cgt	ggc	cgg	gaa	cca	ctg	aca	gat	tta	gtt	cgt	gaa	ctt	gaa	499		
Leu	His	Arg	Gly	Arg	Glu	Pro	Leu	Thr	Asp	Leu	Val	Arg	Glu	Leu	Glu			
120						125						130						
ata	act	gtg	gtg	ata	gac	gat	gtt	ctt	cca	cgg	cgg	gga	gta	gtg	cca	547		
Ile	Thr	Val	Val	Ile	Asp	Ala	Val	Leu	Pro	Pro	Pro	Gly	Val	Val	Pro			
135						140						145						
ggc	aca	tgc	ctg	ccc	aat	tgg	gta	aaa	aat	gga	tat	gta	aga	atg	cgt	595		
Gly	Thr	Leu	Val	His	Asn	Leu	Val	Lys	Glu	Gly	Tyr	Ala	Arg	Met	Arg			
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cct	ggg	act	egg	ggg	tta	gat	gta	ggc	cct	gac	ggc	acc	gtt	caa	ggg	643		
Pro	Gly	Thr	Arg	Gly	Leu	Asp	Val	Ala	Ala	Asp	Gly	Thr	Val	Gln	Gly			
170						175						180						
caa	cga	cat	ttg	gct	gca	gac	aga	cgg	atg	acg	gaa	gac	gtg	gtt	ttg	691		
Gln	Arg	His	Leu	Ala	Ala	Val	Gly	Arg	Met	Thr	Glu	Asp	Val	Val	Leu			
185						190						195						
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Gly	Asn	Asp	Thr	Leu	Ser	Arg	Ser	Leu	His	Asp	Ile	Ile	Pro	Lys	Trp			
200						205						210						
gct	cgt	cga	gtt	atc	cgc	gac	gcg	agg	acg	tat	ccc	gat	agg	gta	cat	787		
Ala	Arg	Arg	Val	Ile	Arg	Asp	Ala	Ser	Thr	Tyr	Pro	Asp	Arg	Val	His			
215						220						225						
ggt	act	cca	cgg	ctc	cgg	gca	cgg	ctg	caa	ccc	tgg	cgc	gaa	aag	ctc	835		
Gly	Thr	Pro	Pro	Leu	Pro	Ala	Arg	Leu	Glu	Pro	Trp	Ala	Glu	Lys	Leu			
230						235						240						245
act	tca	gat	cgg	goc	aca	tgc	cgc	cac	ctg	att	gaa	gaa	ttc	ggg	agt	883		
Thr	Ser	Asp	Pro	Ala	Thr	Cys	Arg	His	Leu	Ile	Glu	Glu	Phe	Gly	Ser			
250						255						260						
cct	gtg	aat	gta	ctc	cat	tca	ggt	tct	atg	cct	cgt	aat	ata	aat	gag	931		
Pro	Val	Asn	Val	Leu	His	Ser	Gly	Ser	Met	Pro	Arg	Asn	Ile	Asn	Glu			
265						270						275						

ttg gtt gac gcc ggc att cag atg ggg gtg gat act cga ata ttt ttt	979
Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp Thr Arg Ile Phe Phe	
280 285 290	
gac cgc aaa ggc aat aag ggt ctt acc ttc gtt gat gcc gtt aaa gac	1027
Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val Asp Ala Val Lys Asp	
295 300 305	
acc ggt cat ggt gta gat gta gcc agt gaa cga gag tta tct cag gtg	1075
Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val	
310 315 320 325	
ctt aat cgt gga gtc cca gga tag cgg atc att cta tcc gca gct acc	1123
Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile Leu Ser Ala Ala Ile	
330 335 340	
aaa ccg gac aga cta tgg gcc tta ggc atc gaa aat ggc gtg atc atc	1171
Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu Asn Gly Val Ile Ile	
345 350 355	
tct gtg gat tgg cgt cat gaa tta gat cgc att tgg gct tgg gtt ggt	1219
Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile Ser Ala Leu Val Gly	
360 365 370	
gac cgc gtt gca cca gtc ggc cct aga gta gct cca gat cct gca gtc	1267
Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala Pro Asp Pro Ala Val	
375 380 385	
tta cct cca act aga ttt ggt tag cgt gct gca gac tgg ggt aat cgg	1315
Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala Asp Trp Gly Asn Arg	
390 395 400 405	
ctt acc gag gtg ata ccc ggc tgg cat att gta ggt ctt cag gtt cag	1363
Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val Gly Leu His Val His	
410 415 420	
ctc cat ggc tat gct gca aaa gac cgt gct ctg gct ctg cag gaa tgt	1411
Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu Ala Leu Gln Glu Cys	
425 430 435	
tgc caa ctc gtc gat tct ctc aga gaa tgc ggc cat tcc cca cag tat	1459
Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly His Ser Pro Gln Phe	
440 445 450	
att gac ctt gga gga ggg ggg cct atg agc tac att gaa tct gag gaa	1507
Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr Ile Glu Ser Glu Glu	
455 460 465	
gat tgg atc cgt tat cca tcc gct aaa tct ggc act tca gcc ggc tat	1555
Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala Thr Ser Ala Gly Tyr	
470 475 480 485	
gcc gaa tcc ttt acg tgg aaa gac gat ccg tta tct aat acg tac ccg	1603
Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu Ser Asn Thr Tyr Pro	
490 495 500	
ttc tat cag acc cca gtg cgc ggt aat tgg ttg aaa gac gtg ctt tct	1651
Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu Lys Asp Val Leu Ser	
505 510 515	

aag ggg gta got cag atg ctc att gac cgg gga ttg cgg tta cac ata 1639  
 Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly Leu Arg Leu His Ile  
 520 525 530

gag cct ggt cga agt tta cta gat ggg tgt ggc gtc act ctt gcc gaa 1747  
 Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly Val Thr Leu Ala Glu  
 535 540 545

ggt cct ttt gtg aaa acg cga agt gac ggg ttg cct cta gtg gga ctg 1795  
 Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu Pro Leu Val Gly Leu  
 550 555 560 565

ggt atg aac cga acc cag tgc cgg act aca tcc gat gat ttt ctc att 1843  
 Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser Asp Asp Phe Leu Ile  
 570 575 580

ggt ccc ctg cat atc act gac ggt gat gta ggc gag gaa atc gaa gca 1891  
 Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly Glu Glu Ile Glu Ala  
 585 590 595

tat cta gta ggt gcc ttc tgc atc gaa gat gag ctg att tta cgc cgg 1939  
 Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu Leu Ile Leu Arg Arg  
 600 605 610

cga atc cgt ttc cgg aca gga gtc aaa cca gga gat atc atc gga att 1987  
 Arg Ile Asn Phe Pro Arg Gly Val Lys Pro Gly Asp Ile Ile Gly Ile  
 615 620 625

gtt aac acc gca gga ttc ttc atg cat atc ttg gaa agt gca tgc cac 2035  
 Phe Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His  
 630 635 640 645

cga atc cgt ttg ggc aca aat gta gtc tgg cgg gag ggg cag tta gac 2083  
 Glu Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp  
 650 655 660

gtt atc gat gag gat taagacataa caattcgcta atc 2121  
 Asp Ile Asp Ala Asp  
 665

C10: 46

C11: 666

C12: PRF

C13: Corynebacterium glutamicum

C100: 46

Met Ile Pro Lys Pro Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu  
 1 5 10 15

Asn Glu Gly Ser Glu Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu  
 20 25 30

Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly  
 35 40 45

Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr  
 50 55 60

Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile  
 65 70 75 80

Gly Phe Asp His	Leu Ala Arg	Glu Met	Glu Arg	Leu Ala	Phe Gly Pro
	85		90		95
Pro Ser Glu Ser	Phe Glu Tyr	Leu Gln	Glu Leu	Val Lys	Ser Gly Val
	100		105		110
Val Asp Ile Thr	His Leu His	Arg Gly	Arg Glu	Pro Leu	Thr Asp Leu
	115		120		125
Val Arg Glu Leu	Glu Ile Thr	Val Val	Ile Asp	Ala Val	Leu Pro Pro
	130		135		140
Pro Gly Val Val	Pro Gly Thr	Leu Val	His Asn	Leu Val	Lys Glu Gly
	145		150		155
Tyr Ala Arg Met	Arg Pro Gly	Thr Arg	Gly Leu	Asp Val	Ala Ala Asp
	160		170		175
Gly Thr Val Gln	Gly Gln Arg	His Leu	Ala Ala	Val Gly	Arg Met Thr
	180		185		190
Glu Asp Val Val	Leu Gly Asn	Asp Thr	Leu Ser	Arg Ser	Leu His Asp
	195		200		205
Ile Ile Pro Lys	Trp Ala Arg	Val Ile	Arg Asp	Ala Ser	Thr Tyr
	210		215		220
Pro Asp Arg Val	His Gly Thr	Pro Pro	Leu Pro	Ala Arg	Leu Glu Pro
	225		230		235
Trp Ala Glu Lys	Leu Thr Ser	Asp Pro	Ala Thr	Cys Arg	His Leu Ile
	240		250		255
Glu Glu Phe Gly	Ser Pro Val	Asn Val	Leu His	Ser Gly	Ser Met Pro
	260		265		270
Arg Asn Ile Asn	Glu Leu Val	Asp Ala	Gly Ile	Gln Met	Gly Val Asp
	275		280		285
Thr Arg Ile Phe	Phe Ala Arg	Lys Ala	Asn Lys	Gly Leu	Thr Phe Val
	290		295		300
Asp Ala Val Lys	Asp Thr Gly	His Gly	Val Asp	Val Ala	Ser Glu Arg
	305		310		315
Glu Leu Ser Gln	Val Leu Asn	Arg Gly	Val Pro	Gly Glu	Arg Ile Ile
	320		330		335
Leu Ser Ala Ala	Ile Lys Pro	Asp Arg	Leu Leu	Ala Leu	Ala Ile Glu
	340		345		350
Asn Gly Val Ile	Ile Ser Val	Asp Ser	Arg Asp	Glu Leu	Asp Arg Ile
	355		360		365
Ser Ala Leu Val	Gly Asp Arg	Val Ala	Arg Val	Ala Pro	Arg Val Ala
	370		375		380
Pro Asp Pro Ala	Val Leu Pro	Pro Thr	Arg Phe	Gly Glu	Arg Ala Ala
	385		390		395
					400

Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val  
 405 410 415  
 Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu  
 420 425 430  
 Ala Leu Gln Glu Cys Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly  
 435 440 445  
 His Ser Pro Gln Phe Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr  
 450 455 460  
 Ile Glu Ser Glu Glu Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala  
 465 470 475 480  
 Thr Ser Ala Gly Tyr Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu  
 485 490 495  
 Ser Asn Thr Tyr Pro Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu  
 500 505 510  
 Lys Asp Val Leu Ser Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly  
 515 520 525  
 Leu Arg Leu His Ile Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly  
 530 535 540  
 Val Thr Leu Ala Glu Val Ala Pro Val Lys Thr Arg Ser Asp Gly Leu  
 545 550 555 560  
 Pro Leu Val Gly Leu Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser  
 565 570 575  
 Asp Asp Phe Leu Ile Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly  
 580 585 590  
 Ala Glu Ile Glu Ala Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu  
 595 600 605  
 Leu Ile Leu Arg Arg Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly  
 610 615 620  
 Asp Ile Ile Gly Ile Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu  
 625 630 635 640  
 Glu Ser Ala Ser His Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro  
 645 650 655  
 Glu Gly Gln Leu Asp Asp Ile Asp Ala Asp  
 660 665

0210 - 47

0211 - 893

0212 - DNA

0213 - *Corynebacterium glutamicum*

0216 -

0217 - CDS

0218 - (101)...(970)

0219 - EXA01393

&lt;400&gt; 17

caaaagcaaa cctgtaatga agatttccat gatcaccatc gtgacctatg gaagtaactta 60  
 agtaaaatga ttgggttctta acatgggtta atatagcttc atg aac ccc att caa 115  
 Met Asn Pro Ile Gln  
 1 5

ctg gac act ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc 163  
 Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala  
 10 15 20

tcc tta gcc ctt tcc att tcc ccc tgg ggg gtg agt cag cgc gtt aaa 211  
 Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys  
 25 30 35

gct ctg gag cat cac gtg ggt cga gtg ttg gta tgg cgc acc caa cgg 259  
 Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro  
 40 45 50

gcc aac gca acc gaa ggc ggt gaa ctg ctt gtg caa gca ggc cgg aaa 307  
 Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys  
 55 60 65

atg gta ttg ctg caa gca gaa act aac ggc caa cta tct gga cgc att 355  
 Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu  
 70 75 80 85

gct gaa atc cgg tta acc atc gcc atc aac gca gat tgg cta tcc aca 403  
 Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr  
 90 95 100

tgg tct cct ccc gtg ttc aac gag tta gct tct tgg ggt gga gca acc 451  
 Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr  
 105 110 115

ctc acg ctg cgc ttg gaa gat gaa gcc cac aca tta tcc ttg ctg cgg 499  
 Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg  
 120 125 130

cgt gga gat gtt tta gga ggc gta acc cgt gaa gct aat ccc gtg ggc 547  
 Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala  
 135 140 145

gga tct gaa gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca 595  
 Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala  
 150 155 160 165

acc ccc caa ttg cgg gat gcc cac atg gtt gat ggg aaa cta gat tgg 643  
 Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp  
 170 175 180

gct ggc atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac 691  
 Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp  
 185 190 195

cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta 739  
 Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val  
 200 205 210

tcc att gtc cgg tgg ggc gaa ggt ttt ggt gag gca att cgc cga ggc 787

Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly  
 215 220 225

ctt ggt tgg aga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa 835  
 Leu Gly Trp Gly Leu Leu Pro Gln Thr Gln Ala Ala Pro Met Leu Lys  
 230 235 240 245

gca aga gaa atg atc ctc ctg gat gag ata ccc att gag aca cgg atg 883  
 Ala Gly Glu Val Ile Leu Leu Asp Gln Ile Pro Ile Asp Thr Pro Met  
 250 255 260

tat tgg caa aga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca 931  
 Tyr Trp Gln Arg Trp Arg Leu Gln Ser Arg Ser Leu Ala Arg Leu Thr  
 265 270 275

gac ccc gtc att gat gca gca atc gag gga ttg cgg cct tagttaacttc 980  
 Asp Ala Val Val Asp Ala Ala Ile Gln Gly Leu Arg Pro  
 280 285 290

tgaagaagggtt cag 993

<210> 42  
 <211> 290  
 <212> PRT  
 <213> Corynebacterium glutamicum

<110> 48  
 Met Asn Pro Ile Gln Leu Asp Thr Leu Leu Ser Ile Ile Asp Gln Gly  
 1 5 10 15

Ser Phe Gln Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val  
 20 25 30

Ser Gln Arg Val Lys Ala Leu Gln His His Val Gly Arg Val Leu Val  
 35 40 45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val  
 50 55 60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Gln Thr Lys Ala Gln  
 65 70 75 80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala  
 85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Gln Val Ala Ser  
 100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr  
 115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu  
 130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg  
 145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp  
 165 170 175



Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys  
180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val  
195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu  
210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala  
225 230 235 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro  
245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser  
260 265 270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu  
275 280 285

Arg Pro  
290

<210> 49  
 <211> 1626  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (131)...(1635)  
 <223> EXA03241

<400> 49  
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aaqthtagcg acttcgcggt aagtcaccta cgttaaata gtc aat act caa tca 115  
 Val Asn Thr Gln Ser  
 1 5

gat tct ggc ggg tct caa ggt gca ggc gcc aca agt cgt act gta tct 163  
 Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr Ser Arg Thr Val Ser  
 10 15 20

att aga acc ctg atc ggc ctg atc atc gga tgg acc gtc ggc gcc gga 211  
 Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly  
 25 30 35

att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc ggc 259  
 Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala  
 40 45 50

atg ctg atc ggc tgg ctg atc gcc ggt gtg ggc atg ttg tcc gta gcc 307  
 Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala  
 55 60 65

ttc gtg ttc cat gtt att gcc cgc cgt aaa cct cac ctg gat tct ggc 355  
 Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly  
 70 75 80 85

gtc tac gca tat ggc cgt gtt gga ttg ggc gat tat gta ggt ttc tcc	403
Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp Tyr Val Gly Phe Ser	
90 95 100	
tcc gct tgg ggt tat tgg ctg ggt tca gtc atc ggc caa ggt ggc tac	411
Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr	
105 110 115	
gca acg tta ttt ttc tcc acg ttg ggc cac tac gta ccg ctg ttt tcc	419
Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser	
120 125 130	
caa gat cat caa ttt gtc tca ggc ttg gca gtt agc gct tgg acc tgg	547
Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp	
135 140 145	
ctg ctg ttt gca gtt gtt tcc cga gga att agc caa gct cct ttc ctg	585
Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser Gln Ala Ala Phe Leu	
150 155 160 165	
aca acg gtc ccc acc ctg gcc aac att ctg cct ctg ttg tgc ttc atc	643
Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Cys Phe Ile	
170 175 180	
atc att gtt caa ttc ttg gcc ttt agc tgg gag aag ttc cct gtt gat	691
Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp	
185 190 195	
tta tgg cgc cgt cat gct gcc gtc ggc agc att ttt gat tag gtc cgc	719
Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp His Val Arg	
200 205 210	
ggc atc atg ttc tac acc gtc tgg gtc ttc atc ggt atc caa ggt gca	787
Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile His Gly Ala	
215 220 225	
tgg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cga gct	835
Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala	
230 235 240 245	
acc gtc att cgt ttt ctg gct gtc ttc ctt ttg ctg ctg ttg att cct	883
Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Val Ser Ile Ser	
250 255 260	
tgg ctg agc ttc ggt gta ctg acc caa caa gag ctg gct ggc tta caa	931
Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro	
265 270 275	
gat aat tcc atc ggc tgg gtc ctg gaa gct att gtt ggt tca tgg ggt	979
Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly	
280 285 290	
gac gca ttg att tgg ttg gct ctg tgt ctt ttg gtt ctt ggc gcc tat	1027
Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr	
295 300 305	
gtg tcc tgg cag atg ctg tgc gca gaa cca ctg ggc ttg atg gca atg	1075
Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met	
310 315 320 325	

gat ggc ctc att cca agc aaa atc ggg gcc atc aac agc cgc ggt got 1123  
Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala  
330 335 340  
gac tgg atg got cag ctg atc too acc atc gtg att cag att ttc atc 1171  
Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile  
345 350 355  
atc att ttc ttc ctc aac gag acc acc tac gtc too atg gtg caa ttg 1219  
Ile Ile Phe Phe Leu Asn Gln Thr Thr Tyr Val Ser Met Val Gln Leu  
360 365 370  
ggt acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg 1267  
Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu  
375 380 385  
gtc ctg ctg gca aca cgt gga aaa gga atc acc cac cca cat gcc ggc 1315  
Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly  
390 395 400 405  
aaa cgt ttt gat gat too ggt cca gag ata too cgc cga gaa aac cgc 1363  
Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser Arg Arg Glu Asn Arg  
410 415 420  
aaa cac ctc atc gtc ggt tta gta gca acc gtg tat tta gtg tgg ctg 1411  
Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu  
425 430 435  
ttt tac got gca gaa cgc cag ttt gtc ctc ttc gga gcc atg gcc atg 1459  
Phe Tyr Ala Ala Gln Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met  
440 445 450  
gtt acc gcc tta atc ccc tac gtg tgg acc agg att tat cgt gcc gaa 1507  
Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu  
455 460 465  
cag gtg ttt aac cgc ttt gaa atc gcc gtg gtt gtt gtc ctg gtc gtt 1555  
Gln Val Phe Asn Arg Phe Gln Ile Gly Val Val Val Val Leu Val Val  
470 475 480 485  
ggt gcc agc gcc gcc gtt att ggt ttg gtc aac gga tca cta tgg ctt 1603  
Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu  
490 495 500  
taaacaccca aaccttcctg cta 1626

0110-30

0111-501

0112-PRT

0113-Corynebacterium glutamicum

0420-30

Val Asn Thr Gln Ser Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr  
1 10 15

Ser Arg Thr Val Ser Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser  
20 25 30

Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val  
35 40 45

Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly  
 50 55 60  
 Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro  
 65 70 75 80  
 His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp  
 85 90 95  
 Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile  
 100 105 110  
 Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr  
 115 120 125  
 Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val  
 130 135 140  
 Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser  
 145 150 155 160  
 Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro  
 165 170 175  
 Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu  
 180 185 190  
 Lys Phe Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile  
 195 200 205  
 Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile  
 210 215 220  
 Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser  
 225 230 235 240  
 Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu  
 245 250 255  
 Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu  
 260 265 270  
 Leu Ala Ala Leu Pro Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val  
 275 280 285  
 Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser  
 290 295 300  
 Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu  
 305 310 315 320  
 Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile  
 325 330 335  
 Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val  
 340 345 350  
 Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val  
 355 360 365

Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe  
 270 375 380

Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr  
 335 390 395 400

His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser  
 405 410 415

Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val  
 420 425 430

Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe  
 435 440 445

Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg  
 450 455 460

Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val  
 465 470 475 480

Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn  
 485 490 495

Gly Ser Leu Ser Leu  
 500

<210> = 51

<211> = 122

<212> = DNA

<213> = *Corynebacterium glutamicum*

<220> =

<221> = CDS

<222> = (101)...(799)

<223> = RXA01394

<400> = 51

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ccattttact taagtaacttc cataggtcac gatggtgata atg gaa atc ttc att 115  
 Met Glu Ile Phe Ile  
 1 5

aca ggt ctg att ttg ggg gcc agt ctt tta ctg tcc atc gga cgg cag 163  
 Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu Ser Ile Gly Pro Gln  
 10 15 20

aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctg att ggc 211  
 Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala  
 25 30 35

ggt ctt ctg gtg tgt tta att tct gac gtc ttt ctg ttc atc gcc ggc 259  
 Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly  
 40 45 50

acc ttg ggc gtt gat ctt ttg tcc aat gcc ggc cgc atc gtg ctg gat 307  
 Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp  
 55 60 65

att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg 355  
 Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met  
 70 75 80 85  
 gca ggc aaa gac gcc atg aca aac aag gtg gaa ggc aca cag atc att 403  
 Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile  
 90 95 100  
 gaa gaa aca gaa aca aac gtg aac gat gac aag cct ttg ggc ggt tgg 451  
 Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr Pro Leu Gly Gly Ser  
 105 110 115  
 ggc ttg gcc aat gac aag cgc aac cgg gtg cgg gtg gag gtg aag gtc 499  
 Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val  
 120 125 130  
 gat aag cag cgg gtt tgg gta aag aac atg ttg atg gca atc gtg ctg 547  
 Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu  
 135 140 145  
 aac tgg ttg aat cgg aat ggc tat ttg gac ggc ttt gtg ttt atc ggc 595  
 Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly  
 150 155 160 165  
 ggc ttc gcc ggc ggc aca tac ggc gac aac gga cgg tgg att ttc gcc gct 643  
 Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala  
 170 175 180  
 ggc cgg ttc ggc gca aac atg aac ttg ttc cgg ctg atg ggt ttc gcc 691  
 Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly  
 185 190 195  
 gca gca gca ttg tca cgc cgg ctg aac aag aac aag atg tgg cgc tgg 739  
 Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp  
 200 205 210  
 atc aac gtc gtc gtg gca gtt gtg atg aac gga ttg gcc atc aac ctg 787  
 Ile Asn Val Val Val Ala Val Met Thr Ala Leu Ala Ile Lys Leu  
 215 220 225  
 atg ttg atg ggt tagttttcgc gggttttgga atc 822  
 Met Leu Met Gly  
 230

1310-52

1311-233

1312-PET

1313-Corynebacterium glutamicum

1400-52

Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu  
 1 5 10 15

Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg  
 20 25 30

Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe  
 35 40 45

Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala

-2010 - 13  
 -2011 - 10-26  
 -2012 - DNA  
 -2013 - *Corynebacterium glutamicum*

000000  
 000000 - CDS  
 000000 - (101)...(1003  
 000000 - EXA00865

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04000 x 50
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ttaaaccccc aaatgagtgga agaaggtaac cttgaactct atg agc aca ggt tta 115
Met Ser Thr Gly Leu
1 5
aca gct aag acc gga gta gag cac ttc ggc acc gtt gga gta gca atg 163
Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr Val Gly Val Ala Met
10 15 20
gtt act cca ttc acg gaa tcc gga gac atc gat atc gct gct ggc cgc 211
Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp Ile Ala Ala Gly Arg
25 30 35

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gaa gtc gog got tat ttg gtt gat aag ggc ttg gat tot ttg gtt ctc	259
Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu Asp Ser Leu Val Leu	
40 45 50	
gog ggc aac aat ggt gaa tcc cca acg aca acc ggc got gaa aaa cta	307
Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu	
55 60 65	
gaa ctg ctc aag ggc gtt cgt gag gaa gtt ggg gat cgg gog aag ctc	355
Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu	
70 75 80 85	
acc ggc ggt gtc gga acc aac aac acg cgg aca tct gtg gaa ctc gog	403
Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala	
90 95 100	
gaa got got got tct got cgc gca gac ggc ctt tta gtt gta aat cct	451
Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro	
115 11 115	
tat tac tcc aag cag agc caa gag gga ttg ctg gog aac ttc ggt gca	499
Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His Phe Gly Ala	
120 125 130	
att got gca gca aac gag gtt cca att tct ctc tat gac att ctt ggt	547
Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly	
135 140 145	
cgg tca ggt att cca att gag tct gat aac atg aga cgc ctg aat gaa	595
Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu	
150 155 160 165	
tca cct acg att ctg gog ctc aag gac gca aag ggt gac ctc gtt gca	643
Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala	
170 175 180	
goc aag tca ttg atc aaa gaa aag gga ctt ggc tgg tat tca ggc gat	691
Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp	
185 190 195	
gac cca cca aac ctt gtt tgg ctt got ttg ggc gga tca ggt ttc att	739
Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile	
200 205 210	
tcc gta att gga cat gca gcc ccc aca gca tca cgt gag ttg tcc aca	787
Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr	
215 220 225	
agc ttc gag gaa ggc gac ctc gtc cgt gog cgg gaa atc aac ggc aaa	835
Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys	
230 235 240 245	
cta tca cag ctg gta got gcc caa ggt cgc ttg ggt gga gtc aac ttg	883
Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu	
250 255 260	
gca aaa got got ctg cgt ctg cag gcc atc aac gta gga gat cct cga	931
Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg	
265 27 275	
ctt cca att atg got cca aat gag cag gaa ctt gag got ctc cga gaa	979



Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu  
 280 285 290

gac atg aaa aaa gct gga gtt ata taaatatgaa tgattccaga aat 1026  
 Asp Met Lys Lys Ala Gly Val Leu  
 295 300

<210> 34

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<240> 34

Met Ser Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr  
 1 5 10 15

Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp  
 2 25 30

Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu  
 35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr  
 50 55 60

Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly  
 65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr  
 85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu  
 10 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu  
 115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu  
 130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met  
 145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys  
 165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala  
 180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly  
 195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu  
 210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg  
 225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu  
 245 250 255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn  
261 265 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu  
275 280 285

Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu  
290 295 300

<210> : 65

<311> : 1071

<212> : DNA

<213> : Corynebacterium glutamicum

<310> :

<311> : CDS

<312> : (101)..(1048)

<313> : EXS02021

<10> : 15

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aaaccttagt taaaacatga tggacgpggt cgattaaaaa atg agt gaa aac att 115  
Met Ser Glu Asn Ile  
1 5

cgcgga gcc caa gca gtt gga atc gca aat att gcc atg gac ggg aac 163  
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr  
10 15 20

atc ctg gac cgc tgg tac cca gaa ccc caa att ctg aac cgc gat cag 211  
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln  
25 30 35

tgcgct gaa cgc tac cca ttg gaa gtg ggc aac aca cgc ctg gga gca 259  
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala  
40 45 50

aac gaa ctg aac cca cgg atg ctg cag ttg gta aaa ctg gac caa gat 307  
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp  
55 60 65

cgc ctg gtc gaa cag gta gca gtc cgc aac gtt atc ccc gat ctg cct 355  
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser  
70 75 80 85

caa cct cca gta gac cgc cac gat gtt tac ctg cgc ctg cac ctg ctt 403  
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu  
90 95 100

ctc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac aac ttg 451  
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu  
105 110 115

gag ctg ctg tcc gac gtg gtg ttg aca aac aag ggc cct tgc ctt cct 499  
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro  
120 125 130

gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctg atc 547

Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile  
 135 140 145  
 cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtc 595  
 His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val  
 150 155 160 165  
 ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt goa 643  
 Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala  
 170 175 180  
 tac ctt gct ccc ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691  
 Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe  
 185 190 195  
 acc tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739  
 Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser  
 200 205 210  
 ggt gtc gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att 787  
 Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile  
 215 220 225  
 cag tcc ccc aga gat gaa cag cgc cgc cgt ttg cag ttg agc atc ggc 835  
 Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly  
 230 235 240 245  
 caa aac tcc aac ttt ggt gtc aga tcc gga atc atc gga ctg agt ctg 883  
 Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu  
 250 255 260  
 pra ccc aat tgc cac atc gga aat aac att gct ttg gat gga gat acc 931  
 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr  
 265 270 275  
 acc att tgg ttc goa gcc gat gag gag tta cgc act atc gac tcc atc 979  
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile  
 280 285 290  
 gaa ggc caa goa aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027  
 Gln Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu  
 295 300 305  
 caa ttt gcc cgc ctg aaa gct cgaccattt tcataaccag tgc 1071  
 Pro Val Ala Arg Leu Lys Ala  
 310 315

0210 - 86

0211 - 316

0212 - PFT

0213 - *Corynebacterium glutamicum*

0400 - 56

Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile  
 1 5 10 15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile  
 20 25 30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr

35	40	45
Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val 50 55 60		
Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val 65 70 75 80		
Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu 85 90 95		
Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His 100 105 110		
Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys 115 120 125		
Gly Pro Cys Leu Pro Gln Asn Phe Glu Trp Val Arg Gly Ala Leu Arg 130 135 140		
Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met 145 150 155 160		
Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg 165 170 175		
Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu 180 185 190		
Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu 195 200 205		
Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly 210 215 220		
Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu 225 230 235 240		
Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile 245 250 255		
Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val 260 265 270		
Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg 275 280 285		
Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu 290 295 300		
Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala 305 310 315		

0010 - 17

0011 - 1245

0012 - DNA

0013 - *Corynebacterium glutamicum*

0020 -

0021 - CDS

&lt;222&gt; (191)..(1273)

&lt;223&gt; EX302157

&lt;400&gt; 57

gggtagaatt ggcaacgatgg tgetgcacgga tgtttttgat cgggagaatt atcctgaagg 60

caacattttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115  
Met Ser Thr Leu Glu  
1 5

aat tgg caa cag gtc att att aat acg tac ggc acc caa caa gtt gag 163  
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu  
10 15 20

ctg gtc tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211  
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val  
25 30 35

tac atc gag ttg ctg gcg ggc atc gca gtc aac gcg ttg ggc caa ggc 259  
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala  
40 45 50

caac tgg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307  
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly  
55 60 65

caac ttc tca aac ttg ttc gca tcc agy caa gtc gtc gag gtc gca gag 355  
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu  
70 75 80 85

gag ttc atc aag cgt ttt tcc ctt gag gac ggc acc cta gcc gcg caa 403  
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln  
90 95 100

aac tgg gtt ttc ttc tgc aac tcc ggc gcc gaa gca aac gaa got got 451  
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Gln Ala Ala  
105 110 115

tac tag att gca cgc ttg act ggt cgt tcc cgg att ctg got gca gtt 499  
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val  
120 125 130

cct ggt ttc caa ggc cgc acc atg ggt tcc ctg gcg ctg act ggc cag 547  
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln  
135 140 145

caa gac aag cgt gaa gcg ttc ctg caa atg caa agc ggt gtc gag ttc 595  
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe  
150 155 160 165

tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac 643  
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn  
170 175 180

caa acg gat gtc got got atc ttc ctg gag caa atc cag ggt gaa acg 691  
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr  
185 190 195

ggc gtt gtt caa gca cct gaa gga ttc ctg aag gca gtc cgc gag ctg 739  
Gly Val Val Pro Ala Pro Gln Gly Phe Leu Lys Ala Val Arg Glu Leu  
200 205 210

tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc 787  
 Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly  
 215 220 225

gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835  
 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val  
 230 235 240 245

ccc tat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883  
 Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile  
 250 255 260

agt gat tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931  
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly  
 265 270 275

aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979  
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala  
 280 285 290

aag cca gtg cag tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027  
 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala  
 295 300 305

acc aag ggc gag ctc ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt 1075  
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val  
 310 315 320 325

cca cac gtc ctt ggc agg ggc ttg atg ttg ggc ggc gtc ctc gag cgc 1123  
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
 330 335 340

tcc ttc gca aag caa gct ctt ctt gat ggt ttt aag cac ggc gtt att 1171  
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
 345 350 355

ttg aat gca cag ggc gac aac att acc cgt ttg acc ccc ccc ctc gtc 1219  
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val  
 360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag acc 1267  
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr  
 375 380 385

atc gca taaaggactc aaacttatga ctt 1296  
 Ile Ala  
 390

0110: 58

0111: 391

0112: FRT

0113: *Corynebacterium glutamicum*

0400: 58

Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly  
 1 5 10 15

Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp  
 20 25 30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn  
 35 40 45  
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln  
 50 55 60  
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val  
 65 70 75 80  
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala  
 85 90 95  
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu  
 100 105 110  
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg  
 115 120 125  
 Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu  
 130 135 140  
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro  
 145 150 155 160  
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys  
 165 170 175  
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro  
 180 185 190  
 Ile Glu Gly Glu Thr Gly Val Val Pro Ala Pro Gln Gly Phe Leu Lys  
 195 200 205  
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp  
 210 215 220  
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln  
 225 230 235 240  
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly  
 245 250 255  
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu  
 260 265 270  
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val  
 275 280 285  
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe  
 290 295 300  
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala  
 305 310 315 320  
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly  
 325 330 335  
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe  
 340 345 350

Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu  
355 360 365

Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys  
370 375 380

Ala Ile Ala Glu Thr Ile Ala  
385 390

#210 - 19

#211 - 1008

#212 - DNA

#213 - *Corynebacterium glutamicum*

#220 -

#221 - CDS

#222 - (151)...(985)

#223 - EX000733

#400 - 19

acggcgaggt tgcgggtatt ggaacgcaca cgaatttgcg gaacacgtgc ggtacctacc 60

gtgaattgt tgaattccaa gagactggcg agggcgcaatc atg agt aat act gaa 115  
Met Ser Asn Thr Ala  
1 5

ggc ccc cgc ggg cgt tcc cat cag gca gac gcc gcg ccg aat caa aag 163  
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys  
10 15 20

gca ccc cat ttc gga cca tat gcc aac agg ctt ttc gga att cta gcc 211  
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Phe Gly Ile Leu Gly  
25 30 35

cat gac cgt aac acc tta att ttt gtt atc ttc cta gcc gtc ctg agc 259  
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser  
40 45 50

gtt gga ctt acc gtc ttg ggc cca tgg ttg ctg ggt aaa gcc acc aac 307  
Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn  
55 60 65

gtg atg ttt gaa gga ttc cta tct aag cgc atg ccg gct ggt gcg tca 355  
Val Val Phe Gln Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser  
70 75 80 85

aag gaa gat atc atc gcc cag ttg cag gct gca ggt aaa cat aat cag 403  
Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln  
90 95 100

gct tcc atg atg gaa gac atg aac ctt gtt cca gcc tca gcc att gat 451  
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp  
105 110 115

ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc 499  
Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu  
120 125 130

atc ggt agc ctg ttg tgc ttg ttc cag gcc cgg atg ctc aac cgc atc 547  
Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile



135	140	145	
gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc			595
Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile			
150	155	160	165
cac cgg cta cgg ctg agc tat ttc gat ttc atc aaa cgt ggt gat ctg			643
His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu			
	170	175	180
ttt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa			691
Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln			
	185	190	195
aaa acc ttg taa cag gcc atc act tcc cta ctg acc gtc atc ggt gtg			739
Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val			
	200	205	210
ttc ctg atg atg ttt atc atc tcc caa ctg ctg gca ctg gtg gcc ctg			787
Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu			
	215	220	225
tta tcc att cgg gtc acc atc gtg gtc act gtg gtg gtt gcc agc cgt			835
Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg			
	230	235	240
taa cag aaa ctc ttt gcc gaa cag tgg aag cag acc ggt att ttg aat			883
Ser Gln Lys Leu Phe Ala Gln Gln Trp Lys Gln Thr Gly Ile Leu Asn			
	245	250	255
ggc cgg ctg gag gaa acc tac tct gcc cac gcc gtg gtt aag gtt ttc			931
Ala Arg Leu Gln Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe			
	260	265	270
gga cac caa aag gat gtt caa gaa gaa ttc gag gaa gaa aat caa gct			979
Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala			
	275	280	285
tgt cta taaggccagc ttctgttccc agt			1008
Cys Val			
	290		

(210)- 60

(211)- 336

(212)- 557

(213)- *Corynebacterium glutamicum*

(400)- 60

Met Ser Asn Thr Ala Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala

1

5

10

15

Ala Pro Asn Gln Lys Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu

20

25

30

Phe Gly Ile Leu Gly His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe

35

40

45

Leu Ala Val Leu Ser Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu

50

55

60

Gly Lys Ala Thr Asn Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met  
 65 70 75 80  
 Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala  
 85 90 95  
 Gly Lys His Asn Gln Ala Ser Met Met Glu Asp Met Asn Leu Val Pro  
 100 105 110  
 Gly Ser Gly Ile Asp Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val  
 115 120 125  
 Ile Gly Ala Tyr Leu Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg  
 130 135 140  
 Met Leu Asn Arg Ile Val Gln Ser Ala Met His Arg Leu Arg Met Glu  
 145 150 155 160  
 Val Gln Gln Lys Ile His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile  
 165 170 175  
 Lys Arg Gly Asp Leu Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile  
 180 185 190  
 Lys Gln Ser Leu Gln Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu  
 195 200 205  
 Thr Val Ile Gly Val Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu  
 210 215 220  
 Ala Leu Val Ala Leu Val Ser Ile Pro Val Thr Ile Val Val Thr Val  
 225 230 235 240  
 Val Val Ala Ser Arg Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln  
 245 250 255  
 Thr Gly Ile Leu Asn Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala  
 260 265 270  
 Val Val Lys Val Phe Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu  
 275 280 285  
 Glu Gln Asn Gln Ala Cys Val  
 290 295

3110 - 61  
 3111 - 426  
 3112 - DNA  
 3113 - Corynebacterium glutamicum

3120 -  
 3121 - CDS  
 3122 - (1) .. (426)  
 3123 - RXC00861

3400 - 61  
 atg gct cct cac aag gtc atg ctg att acc act ggt act cag ggt gag 48  
 Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu  
 1 5 10 15

cct atg gct ggc ctg tct cgc atg ggc cgt cgt gag cac cga cag atc 96  
 Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile  
                   20                  25                  30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca 144  
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro  
                   35                  40                  45

ggt aac gaa gaa gca atg ttc ggt gtc atc aac atg ctg gct cag atc 192  
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile  
                   50                  55                  60

ggt cca act gtt gtt aac ggt cgc gac gcc aag gtg cac aac tgc ggc 240  
 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly  
                   65                  70                  75                  80

cag cgc tac tcc gga cag ctg ttg ttc ttg tac aac gcc gct cgt ccg 288  
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro  
                   85                  90                  95

aac aac gct atg cct ctc cag ggc gag tgg ccc cag ctg cgc gcc aac 336  
 Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn  
                   100                  105                  110

aag caa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt 384  
 Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu  
                   115                  120                  125

gta caa aac ggt gtt ctg gtt gat atg gtc aac ggt cgc gca 426  
 Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala  
                   130                  135                  140

&lt; 10 - 62

&lt; 11 - 142

&lt; 12 - PRT

< 13 - *Corynebacterium glutamicum*

&lt; 100 - 62

Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu  
                   1                  10                  15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile  
                   20                  25                  30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro  
                   35                  40                  45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile  
                   50                  55                  60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly  
                   65                  70                  75                  80

His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro  
                   85                  90                  95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn  
                   100                  105                  110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu

115	120	125	
Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala			
130	135	140	
4210 - 63			
4211 - 1066			
4212 - DNA			
4213 - Corynebacterium glutamicum			
4220 -			
4221 - CDS			
4222 - (101)..(1066)			
4223 - EXC10866			
4400 - 63			
gaat aaaggt aggagatcct cgaattccaa ttatggctcc aatgagcag gaatttgagg 60			
cct ccaga agaatgaaa aaagctggag ttctataaat atg aat gat tcc cga			115
			Met Asn Asp Ser Arg
			5
at cgc gcc cgg aag gtt acc cgc aag gcg gcc cca cca gaa gct ggt			163
Asn Arg Gly Arg Lys Val Thr Asn Lys Ala Gly Pro Pro Gln Ala Gly			
10			15 20
cct aac aac cat ctg gat acc cct gtc ttt cag gaa cca gat gct tcc			211
Gln Gln Asn His Ser Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser			
25			30 35
cct aac cag agc gct gta aac gct gag acc ggc gga aac gac aat cgg			269
Ser Asn Gln Ser Ala Val Lys Ala Gln Thr Ala Gly Asn Asp Asn Arg			
40			4 50
at cct gcg caa gct gct caa gga tcc caa gat tct cag ggt tcc cag			307
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln			
55			60 65
aac cct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac			385
Asn Ala Gln Gly Ser Gln Asn Arg Gln Ser Gly Asn Asn Asn Arg Asn			
70			75 80 85
cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga			403
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly			
90			95 100
aac gcc aat gag ggt gcg aac aac aac agc ggt aac cag aac cgt cag			451
Asn Ala Asn Gln Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln			
115			110 115
ggc gga aac cgt ggt aac cgc ggt gcc gga cgc cga aac gtt gtt aag			499
Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys			
120			125 130
tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag			547
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Gln Pro Pro Lys			
135			140 145
gca ccg gca aac ggt ctg cgt att tac gca ctt ggt gcc att tcc gaa			595
Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu			

150	155	160	165	
atc tgt cgc aac atg acc gty ttt gag tac aac aac cgt ctg ctc atc				643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile				
170		175	180	
gtg aac tgt ggt gtg ctc ttc cca tct tca ggt gag cca ggc gtt gac				691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp				
185	190	195		
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc				739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val				
200	205	210		
gat cca ttg gtg gtt act cac gga cac gaa gac cac att ggt gct att				787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile				
215	220	225		
ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt				835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg				
230	235	240	245	
ttc acc ttg gat ctg att gca gct aag tgt aag gaa cac cgt cag cgt				883
Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg				
250	255	260		
ccg aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg				931
Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro				
265	270	275		
ttc acc att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt				979
Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu				
280	285	290		
ggc att gat atc aag act cct gct ggt ttg gtc atc cac acc ggt gac				1027
Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp				
295	300	305		
atc aag ctg gat cag act cct cct gat gga cgc cca act				1066
Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr				
310	315	320		

\*210-64

\*211-122

\*212-ERT

\*213-Corynebacterium glutamicum

\*400-64

Met	Asn	Asp	Ser	Arg	Asn	Arg	Gly	Arg	Lys	Val	Thr	Arg	Lys	Ala	Gly
1					5				10					15	

Pro	Pro	Glu	Ala	Gly	Gln	Glu	Asn	His	Leu	Asp	Thr	Pro	Val	Phe	Gln
		20						25					30		

Ala	Pro	Asp	Ala	Ser	Ser	Asn	Gln	Ser	Ala	Val	Lys	Ala	Glu	Thr	Ala
		35					40					45			

Gly	Asn	Asp	Asn	Arg	Asp	Ala	Ala	Gln	Gly	Ala	Gln	Gly	Ser	Gln	Asp
	50					55				60					

Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly  
 65 70 75 80  
 Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly  
 85 90 95  
 Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly  
 100 105 110  
 Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg  
 115 120 125  
 Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu  
 130 135 140  
 Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu  
 145 150 155 160  
 Gly Gly Ile Ser Gln Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn  
 165 170 175  
 Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly  
 180 185 190  
 Gln Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp  
 195 200 205  
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp  
 210 215 220  
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro  
 225 230 235 240  
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys  
 245 250 255  
 Ser His Arg Gln Arg Pro Lys Leu Ile Gln Val Asn Glu Gln Ser Asn  
 260 265 270  
 Gln Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser  
 275 280 285  
 Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val  
 290 295 300  
 Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg  
 305 310 315 320  
 Pro Thr

<210 - 65  
 <211 - 1547  
 <212 - DNA  
 <213 - Corynebacterium glutamicum

<214 -  
 <215 - CD3  
 <216 - (101...1594)  
 <223 - EXC02095

&lt;400&gt; 65

ctctctttggt cctctcctcca cccatttttta agtactcaag acccttcscac cagaaaggat 60

tactcctccca acaggtctcaa aaatactgaa aggcctcaccc atg aaa act gag caa 115  
Met Lys Thr Glu Gln  
1 5

tcc caa aaa gca caa tta gcc cct aag aaa gca cct gaa aag cca caa 163  
Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala Pro Glu Lys Pro Gln  
10 15 20

cgc atc cgc caa ctt att tcc gtg ggc tgg cag cga cct tgg ctg acc 211  
Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln Arg Pro Trp Leu Thr  
25 30 35

tca ttc acc gta atc agc gct tta gct gca aag ttg ttt gaa ctt aca 259  
Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr Leu Phe Glu Leu Thr  
40 45 50

ctt cct ctt ttg acc ggt ggc gcc atc gat atc ggc ctg gga aat acc 307  
Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile Ala Leu Gly Asp Thr  
55 60 65

gga cat act tta acc act gac ctg ctg gac cag ttc act ccg agt gga 355  
Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg Phe Thr Pro Ser Gly  
70 75 80 85

tta agc ggc ttg acc agc gtc att gcc ctt atc gtg ctt ctg ggc ttg 403  
Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu  
90 95 100

ctt agc cat gcc agt caa ctt gga cgg cga ttc acc gca ggc aag ctg 451  
Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr Thr Ala Gly Lys Leu  
105 110 115

agc atg ggc gta cag cat gat gtc cgg ctt aaa acc atg cgc tca ttg 499  
Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu  
120 125 130

cag aac ctg gat ggg cca ggt cag gac tct att cgc aca ggc caa gta 547  
Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val  
135 140 145

gtc agt cgg tcc att tgg gat atc aac atg gtg caa agc ctt gtg ggc 595  
Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala  
150 155 160 165

atg ttg ccg atg ttg atc gga aat gtg gtc aag ctt gtg ctg act ttg 643  
Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu  
170 175 180

gtg atc atg ctg gct att tcc ccg ccg ctg aac atc atc atc gct gca gtg 691  
Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val  
185 190 195

ttg gtg cct ttg ctg ttg tgg gcc gtg gcc tat tgg cga aaa ggc ctt 739  
Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu  
200 205 210

ttt ggc tcc acg tgg tgg gcc cag caa aag gct ggc gat ctg acc act 787

Phe	Ala	Ser	Thr	Trp	Ser	Ala	Gln	Gln	Lys	Ala	Ala	Asp	Leu	Thr	Thr	
215						220				225						
cat	gtg	gaa	gaa	act	gtc	acc	ggg	atc	ggc	gtg	gtc	aag	gca	ttt	gcg	835
His	Val	Glu	Glu	Thr	Val	Thr	Gly	Ile	Arg	Val	Val	Lys	Ala	Phe	Ala	
230					235				240					245		
cag	gaa	gac	ggc	gag	acc	gac	aaa	tgg	gat	ctc	acc	gga	cgt	cag	tta	883
Gln	Glu	Asp	Arg	Glu	Thr	Asp	Lys	Leu	Asp	Leu	Thr	Ala	Arg	Glu	Leu	
				250				255						260		
ttt	goc	cag	ggc	atg	ggc	act	gaa	cgt	ctg	acc	gca	aag	ttc	ctc	ggc	931
Phe	Ala	Gln	Arg	Met	Arg	Thr	Ala	Arg	Leu	Thr	Ala	Lys	Phe	Ile	Pro	
				265				270					275			
atg	gtt	cag	cag	ttt	ggc	cag	ttt	gct	tgg	gtg	ctc	aac	att	gtt	ggc	979
Met	Val	Gln	Gln	Leu	Pro	Gln	Leu	Ala	Leu	Val	Val	Asn	Ile	Val	Gly	
		281					285					290				
ggg	ggc	tat	gtg	goc	atg	act	ggt	cac	ata	acc	gtg	ggc	acc	ttt	gtg	1027
Gly	Gly	Lys	Leu	Ala	Met	Thr	Gly	His	Ile	Thr	Val	Gly	Thr	Phe	Val	
295					300						305					
ggg	ttt	tat	acc	tat	ctc	act	aga	tgg	tgg	ggg	gtg	ggt	agg	acc	gtg	1075
Ala	Phe	Ser	Ser	Tyr	Leu	Thr	Ser	Leu	Ser	Ala	Val	Ala	Arg	Ser	Leu	
310					315					320					325	
cgg	ggc	atg	ctc	atg	ggc	gtg	cag	tgg	ggg	gtg	tct	tct	gtg	cag	ggc	1123
Ser	Gly	Met	Leu	Met	Arg	Val	Gln	Leu	Ala	Leu	Ser	Ser	Val	Ile	Arg	
				330				335						340		
ctc	ttt	gaa	gaa	att	cat	ttt	cag	cct	gaa	aga	acc	gat	cct	gca	cac	1171
Ile	Phe	Gln	Val	Ile	Asp	Leu	Gln	Pro	Gln	Arg	Thr	Asp	Pro	Ala	His	
			345				350						355			
acc	gtg	tca	ttt	acc	gac	act	acc	gtg	ggg	gtg	tgg	tta	aac	aac	gta	1219
Pro	Leu	Ser	Leu	Pro	Asp	Thr	Pro	Leu	Gly	Leu	Ser	Phe	Asn	Asn	Val	
		360					365					370				
gat	ttc	cgt	ggg	att	ctc	aac	ggt	ttt	cag	gtg	ggt	gtt	cag	goc	ggg	1267
Asp	Phe	Arg	Gly	Ile	Leu	Asn	Gly	Phe	Gln	Leu	Gly	Val	Gln	Ala	Gly	
		375				380					385					
gaa	acc	gtt	gtg	tgg	gtg	ggc	cct	cga	ggg	tca	ggc	aag	acc	atg	gct	1315
Gln	Thr	Val	Val	Leu	Val	Gly	Pro	Pro	Gly	Ser	Gly	Lys	Thr	Met	Ala	
390					395				400					405		
gtg	cag	ctt	gct	ggc	aac	ttt	tat	cac	cga	gac	agg	ggc	cac	atc	ggc	1363
Val	Gln	Leu	Ala	Gly	Asn	Phe	Tyr	Gln	Pro	Asp	Ser	Gly	His	Ile	Ala	
				410				415						420		
ttt	gat	agg	aac	ggc	cac	ggc	act	ggc	ttc	gac	cac	ctc	acc	cac	agg	1411
Phe	Asp	Ser	Asn	Gly	His	Arg	Thr	Arg	Phe	Asp	Asp	Leu	Thr	His	Ser	
			425				430						435			
gat	atc	ggc	agg	aac	ctc	atc	ggg	gtt	ttt	gat	cag	cgg	ttc	ttg	tac	1459
Asp	Ile	Arg	Arg	Asn	Leu	Ile	Ala	Val	Phe	Asp	Glu	Pro	Phe	Leu	Tyr	
		440					445					450				
tcc	tcc	tcc	ata	cgg	cga	gaa	cac	ctc	gat	ggg	ttt	gga	tgt	cag		1504
Ser	Ser	Ser	Ile	Pro	Arg	Glu	His	Leu	Asp	Gly	Phe	Gly	Cys	Gln		



455 460 465  
 tgatgagcaq atcgaacacg cag 1527

02100 66  
 02110 468  
 02120 PRT  
 02130 Corynebacterium glutamicum

04000 66  
 Met Lys Thr Glu Gln Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala  
 1 5 10 15  
 Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln  
 20 25 30  
 Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr  
 35 40 45  
 Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile  
 50 55 60  
 Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg  
 65 70 75 80  
 Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile  
 85 90 95  
 Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr  
 100 105 110  
 Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys  
 115 120 125  
 Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile  
 130 135 140  
 Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val  
 145 150 155 160  
 Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys  
 165 170 175  
 Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr  
 180 185 190  
 Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr  
 195 200 205  
 Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala  
 210 215 220  
 Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val  
 225 230 235 240  
 Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu  
 245 250 255  
 Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr  
 260 265 270

Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val  
 275 280 285

Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr  
 290 295 300

Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala  
 305 310 315 320

Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu  
 325 330 335

Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg  
 340 345 350

Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu  
 355 360 365

Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu  
 370 375 380

Gly Val Gln Ala Gly Gln Thr Val Val Leu Val Gly Pro Pro Gly Ser  
 385 390 395 400

Gly Gly Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp  
 405 410 415

Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp  
 420 425 430

Asp Ser Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp  
 435 440 445

Ile Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly  
 450 455 460

Phe Gly Cys Gln  
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 <112> DNA  
 <113> Corynebacterium glutamicum

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 <112> (14)..(272)  
 <113> EX003135

<110>  
 <111> misc\_feature  
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 <113> n = a, c, t, or g

<110> 67  
 agggcccaac cgttcagacc agcgggtttct ctgaggatgc aaagtccatg atgggtnagg 60  
 tcaactgagct gtccgaaacc acc atg aat gat ctt gca gct gaa ggt gaa aac 113  
 Met Asn Asp Leu Ala Ala Glu Gly Glu Asn

	1	5	10	
gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc				161
Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe				
	15	20	25	
gtc cag cag aag tgg aag cgc cag cgc gtc atc atg cca acc gtc att				209
Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile				
	30	35	40	
cgc atg act gag gaa acc acg cac atc ggt gac gat gag gtt cgc gct				257
Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala				
	45	50	55	
cca cgc gag tcc ctg taaaagcatt tcgttttttcg acg				295
Ser Arg Glu Ser Leu				
	60			

010 - 48

011 - 48

012 - EEF

013 - Corynebacterium glutamicum

0400 - 68

Met Asn Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val			
1	5	10	15

Trp Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys			
20	25	30	

Arg Glu Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr			
35	40	45	

Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu			
50	55	60	

010 - 68

011 - 1171

012 - DNA

013 - Corynebacterium glutamicum

0100

0101 - CDS

0102 - (101)...(1147)

0103 - EXA00115

0100 - 69

tgattctcg agtctgtaca ccttgatca aagcccgagt gtccgtaga ttaactttgt 60

gtatattgt gaactacac ccatactgtt aggagttttc atg ctc gac aat agt	115
Met Leu Asp Asn Ser	
1	5

ttt tac acc gca gag gtt cag ggc cca tac gaa acc gct tcc att ggc	163	
Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly		
10	15	20

agg ctc gaa ctc gaa gaa ggg ggt gtg att gag gat tgc tgg ttg gct	211
Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala	

25	30	35	
tac gct aca gct gga aag ctc aac gag gac aag tcc aac gcc atc ctc			259
Tyr Ala Thr Ala Gly Thr Leu Asn Gln Asp Lys Ser Asn Ala Ile Leu			
40	45	50	
att cgg aag tgg tac tcc gga acc cat cag acc tgg ttc cag cag tac			307
Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr			
55	60	65	
atc ggc act gat cat ggg ctg gat cca tca aag tat ttc atc atc tcc			355
Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser			
70	75	80	85
atc aac caa atc ggt aat ggt ttg tgg ttc tcc cat gcc aac acg gct			403
Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala			
90	95	100	
gat gac agc atc tcc aag tcc aag ttc cag aat gtt cgc att ggt gat			451
Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp			
105	110	115	
gat gtc gtt gcc cag gac cgg ctc ttg cgc caa gag ttc ggt att acc			499
Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Gln Pro Gly Ile Thr			
120	125	130	
gag ctg ttc gcc gtc gtt agt ggt tcc aag ggt gag cag caa acc tat			547
Gln Leu Phe Ala Val Val Gly Gly Ser Met Gly Ala Gln Gln Thr Tyr			
135	140	145	
gag tgg att gtt cgc ttc cat gac caa ttc cat cgc gca gct cgg atc			595
Gln Trp Ile Val Arg Pro Pro Asp Gln Val His Arg Ala Ala Pro Ile			
150	155	160	165
ggg gcc act ggg aag aac act cat cat ttc atc ttc aac cag act			643
Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe Ile Phe Thr Gln Thr			
170	175	180	
ctt aat gag acc gtt gag gcc gat cca ggg ttc aat ggc gcc gaa tac			691
Leu Asn Gln Thr Val Gln Ala Asp Pro Gly Phe Asn Gly Gly Gln Tyr			
185	190	195	
tcc tcc cat gaa gag gta gcc gat gga att cgc cgt caa tcc cat ctt			739
Ser Ser His Gln Gln Val Ala Asp Gly Leu Arg Arg Gln Ser His Leu			
200	205	210	
tgg gct gcc atg gga ttc tcc aca gag ttc tgg aag cag gac gca tgg			787
Trp Ala Ala Met Gly Phe Ser Thr Gln Phe Trp Lys Gln Gln Ala Trp			
215	220	225	
cgt cgc ctg gga ctt gaa agt aag gag tca gtg ctc ggc gac ttc ctg			835
Arg Arg Leu Gly Leu Gln Ser Lys Gln Ser Val Leu Ala Asp Phe Leu			
230	235	240	245
gat cgg ctg ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct			883
Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala			
250	255	260	
tgg aag tgg cag cat ggc gat gtc tct cgc cac acc ggc gcc gac ttg			931
Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu			
265	270	275	

gca gag got ott ggc cga gtg aag got aag acc ttc gtt atg ccc atc 979  
 Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile  
 230 235 290  
 ago gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca 1027  
 Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala  
 295 300 305  
 ctg atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cag 1075  
 Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His  
 310 315 320 325  
 ctt ggg cct ctt aac gtc cct gag aat ttc atc cca cag atc gac aaa 1123  
 Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys  
 330 335 340  
 aat ctg aaa gag ctg ttc gag agc taaacctga tgcacagag cct 1170  
 Asn Leu Lys Glu Leu Phe Glu Ser  
 345

&lt;210&gt; 70

&lt;211&gt; 349

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;100&gt; 70

Met Leu Asp Asn Ser Phe Tyr Thr Ala Gln Val Gln Gly Pro Tyr Glu  
 1 5 10 15  
 Thr Ala Ser Ile Gly Arg Leu Glu Leu Gln Gln Gly Gly Val Ile Glu  
 20 25 30  
 Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys  
 35 40 45  
 Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr  
 50 55 60  
 Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys  
 65 70 75 80  
 Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser  
 85 90 95  
 Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn  
 100 105 110  
 Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln  
 115 120 125  
 Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly  
 130 135 140  
 Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His  
 145 150 155 160  
 Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe  
 165 170 175

Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe  
180 185 190

Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg  
195 200 205

Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp  
210 215 220

Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val  
225 230 235 240

Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr  
245 250 255

Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His  
260 265 270

Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr  
275 280 285

Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys  
290 295 300

Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu  
305 310 315 320

Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile  
325 330 335

Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser  
340 345

<110> 71

<111> 1254

<112> DNA

<113> Corynebacterium glutamicum

<120>

<121> CDS

<122> 101...1231

<123> EXN00403

<400> 71

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aagtttttagt ctgtctccacc cagaacaggc gggttttttc atg ccc acc ctc ggc 115  
Met Pro Thr Leu Ala  
1 5

cct tca ggt caa ctt gaa atc caa ggc atc ggt gat gtc tcc acc gaa 163  
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu  
10 15 20

goc gga gga atc att aca aac gct gaa atc goc tat caa cgc tgg ggt 211  
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly  
25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259  
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu

40	45	50	
cac gcc ctc act gga gat tcc aac gca gcc gat tgg tga gct gac ttg His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu 55 60 65			307
ctc ggt ccc gcc aaa gcc atc aac act gat act ttc tgc gtg atc tgt Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys 70 75 80 85			355
acc aac gtc atc ggt ggt tga aac ggt tcc acc gga cct ggc tcc atg Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met 90 95 100			403
cat cca gat gga aat ttc tgg ggt aac ggc ttc ccc gcc acg tcc att His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile 105 110 115			451
agt gat cag gta aac gcc gta aaa caa ttc ctc gac gcc ctc ggc atc Arg Asp Gln Val Asn Ala Gln Lys Gln Phe Leu Asp Ala Leu Gly Ile 120 125 130			499
acc acg gtc gcc gca gta ctt ggt ggt tcc atg gat ggt gcc ggc acc Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr 135 140 145			547
cta gag tgg gcc gca atg ttc cca gaa act gtt gac gcc gct gat gtc Leu Gln Trp Ala Ala Met Tyr Pro Gln Thr Val Gly Ala Ala Ala Val 150 155 160 165			595
ctt gaa gtt tct gca cgc ggt agc gcc tgg caa atc ggt att caa tcc Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser 170 175 180			643
gcc caa att aag gag att gaa aac gac cac caa tgg caa gaa ggc aac Ala Gln Ile Lys Ala Ile Gln Asn Asp His His Trp His Gln Gly Asn 185 190 195			691
tac tac gaa tcc gcc tgc aac cca gcc acc gga ctc ggt gcc gcc gga Tyr Tyr Gln Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg 200 205 210			739
cgc atc gcc cac ctc acc tac cgt ggt gaa cta gaa atc gac gaa cgc Arg Ile Ala His Leu Thr Tyr Arg Gly Gln Leu Gln Ile Asp Gln Arg 215 220 225			787
ttc ggt acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc Phe Gly Thr Lys Ala Gln Lys Asn Gln Asn Pro Leu Gly Pro Tyr Arg 230 235 240 245			835
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac tgg gac tac caa gca Lys Pro Asp Gln Arg Phe Ala Val Gln Ser Tyr Leu Asp Tyr Gln Ala 250 255 260			883
gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gta tgg ctc acc Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr 265 270 275			931
gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn 280 285 290			979

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027  
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075  
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc aac 1123  
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
 330 335 340

gat ggt ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171  
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
 345 350 355

ctc ctc agc ctc atc tcc cca gac gaa gac aac cct tgg acc tac atc 1219  
 Phe Phe Ser Leu Ile Ser Pro Asp Gln Asp Asn Pro Ser Thr Tyr Ile  
 360 365 370

gag ctc tac atc taataggtat ttacgacaaa tag 1254  
 Gln Phe Tyr Ile  
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<.10> 72

<.11> 177

<.12> PRT

<.13> Corynebacterium glutamicum

<.100> 72

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly  
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala  
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
 100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
 115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
 130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
 145 150 155 160



Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
 165 170 175  
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
 180 185 190  
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
 195 200 205  
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
 210 215 220  
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Gln Asn Pro  
 225 230 235 240  
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Gln Ser Tyr  
 245 250 255  
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
 260 265 270  
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
 275 280 285  
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
 290 295 300  
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
 305 310 315 320  
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
 325 330 335  
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
 340 345 350  
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
 355 360 365  
 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile  
 370 375

00100: 73

00110: 1210

00120: DNA

00130: Corynebacterium glutamicum

00200:

00210: CDS

00220: (101)..(1210)

00230: FFXA00463

04000: 73

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aagtttttagt cttgttcacc cagaacagge gggtattttc atg ccc acc ctc gcc 115  
 Met Pro Thr Leu Ala  
 1 5

cct tca ggt caa ctt gaa atc caa ggc atc ggt gat gtc too acc gaa	163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu	
10 15 20	
goc gga gca atc att aca aac gct gaa atc goc tat cac cgc tgg ggt	211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly	
25 30 35	
gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtc ctc atc gaa	259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu	
40 45 50	
cac ggc ctc aat gga gat tcc aac gca gcc gat tgg tgg gct gat ttg	307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu	
55 60 65	
ctc ggt ccc ggc aaa gcc atc aac aat gat att tac tgc gtg atc tgt	355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys	
70 75 80	
acc aac gtc atc ggt ggt ttc aac ggt tcc aac gga cct ggc tcc atg	403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met	
85 90 95 100	
cac cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc aag tcc att	451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile	
105 110 115	
cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc aag gtc gcc gca gta ctt ggt ggt tcc atc ggt ggt gcc cga acc	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gct	595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val	
150 155 160 165	
ctt gca gtt tat gca cgc gcc agc gcc tgg caa atc ggc att caa too	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
goc caa att aag ggc att gaa aac gac cac cac tgg cac gaa ggc aac	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn	
185 190 195	
tac tac gaa too ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
cgc ctc gcc cac ctc aac tac cgt ggt gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa too tac ttg gac tac caa gca	883

Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala  
 250 255 260  
 gac aag cta gta bag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931  
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr  
 265 270 275  
 gac gcc ctc aac cgc cac gac att ggt ggc gac cgc gga ggc ctc aac 979  
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn  
 280 285 290  
 aag gca ctc gaa tcc atc aaa gtt cca gtc att gtc gca ggc gta gat 1027  
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp  
 295 300 305  
 acc gat att ttg tac ccc tac cac bag caa gaa cac ctc tcc aga aac 1075  
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn  
 310 315 320 325  
 atg cga aat cta atg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123  
 Met Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His  
 330 335 340  
 gat cct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtc agg aac 1171  
 Asp Ala Phe Leu Thr Gln Ser Arg Gln Met Asp Arg Ile Val Arg Asn  
 345 350 355  
 ttc ttc agc ctc atc tcc cca gac aac gac aac cct tcc 1210  
 Phe Phe Ser Leu Ile Ser Pro Asp Gln Asp Asn Pro Ser  
 360 365 370

<10> 74

<11> 170

<12> PRT

<13> Corynebacterium glutamicum

<400> 74

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 Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn  
 35 40 45  
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp  
 50 55 60  
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile  
 65 70 75 80  
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr  
 85 90 95  
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe  
 100 105 110  
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu  
 115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met  
 130 135 140  
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val  
 145 150 155 160  
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln  
 165 170 175  
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His  
 180 185 190  
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly  
 195 200 205  
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu  
 210 215 220  
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro  
 225 230 235 240  
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr  
 245 250 255  
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser  
 260 265 270  
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp  
 275 280 285  
 Asp Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu  
 290 295 300  
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu  
 305 310 315 320  
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val  
 325 330 335  
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp  
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 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn  
 355 360 365  
 Pro Ser  
 370

<110> 75  
 <111> 687  
 <112> DNA  
 <113> Corynebacterium glutamicum

<120>  
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 <122> (101)..(664)  
 <123> EXS03158

<400> 75

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 Leu His Ser Thr Thr  
 1 5  
 aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163  
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr  
 10 15 20  
 atc gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211  
 Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile  
 25 30 35  
 gaa cgc atc cca tca gtt ttc gat gaa tac ctg acc gac cgt ggc ctg 259  
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu  
 40 45 50  
 aag acc ctt gaa gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307  
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys  
 55 60 65  
 atc ggc gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctg tac 355  
 Ile Ala Glu Phe Leu Ser Asp Pro Glu Val Ser Thr Val Leu Tyr  
 70 75 80 85  
 cca tgt ctg aag aac cac cca ggc cac gaa gtc gca ggc aag cag atg 403  
 Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met  
 90 95 100  
 aag ggc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451  
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu  
 105 110 115  
 gaa gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499  
 Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu  
 120 125 130  
 ttc ctg ggt ggc gtg gaa tcc ctg ctg gag cac cca gca acc atg acc 547  
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr  
 135 140 145  
 cac cag tca ggt gcc ggc tct cag ctg gag gtt ccc cgc gac ctg gtg 595  
 His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val  
 150 155 160 165  
 ctc atc tcc att ggt att gaa gac att gaa gac ctg ctg gca gat gtc 643  
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val  
 170 175 180  
 gag cag gcc ctg aat aac ctt tagaaaactat ttggcggcaa gca 687  
 Glu Gln Ala Leu Asn Asn Leu  
 185

&lt;110&gt; 76

&lt;111&gt; 188

&lt;112&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 76

Leu His Ser Thr Thr Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly  
 1 5 10 15  
 Gly Leu Val Gly Thr Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe  
 20 25 30  
 Met Gln Gly Gly Ile Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu  
 35 40 45  
 Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys  
 50 55 60  
 Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val  
 65 70 75 80  
 Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val  
 85 90 95  
 Ala Ala Lys Glu Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe  
 100 105 110  
 Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu  
 115 120 125  
 Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His  
 130 135 140  
 Pro Ala Thr Met Thr His Glu Ser Ala Ala Gly Ser Gln Leu Glu Val  
 145 150 155 160  
 Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp  
 165 170 175  
 Leu Leu Ala Asp Val Glu Glu Ala Leu Asn Asn Leu  
 180 185

0101: 77  
 0111: 117  
 0121: DNA  
 0131: Corynebacterium glutamicum

0101: 77  
 0111: CDS  
 0121: (1) .. (124)  
 0131: FRXA00254

0101: 77  
 atg cca cta aaa ctg ggc gca cac gca gtc ttg cac tcc acc acc aag 48  
 Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys  
 1 5 10 15  
 tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac 96  
 Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn  
 20 25 30  
 gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga 144  
 Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly  
 35 40 45  
 ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt gcc ctg aag 192

Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys  
 50 55 60  
 acc att gaa gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc 240  
 Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile  
 65 70 75 80  
 gag gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctg tac cca 288  
 Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro  
 85 90 95  
 ggt ctg aag aac cac cca ggc cac gaa gtc gca gag aag cag atg aag 336  
 Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys  
 100 105 110  
 cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa gca 384  
 Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala  
 115 120 125  
 gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag tcc 432  
 Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser  
 130 135 140  
 ctg ggt ggc gtg gaa tcc ctg ctg gag cac cca gca acc atg acc cac 480  
 Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His  
 145 150 155 160  
 gag tca gct gcc ggc tct cag ctg gag gtt ccc cgc gag ctg gtg ccc 528  
 Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg  
 165 170 175  
 ttc tcc att ggt att gaa gac att gaa gag ctg ctg gca gat gtc gag 576  
 Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Gln  
 180 185 190  
 gag gcc ctg act aac att tagaaaatat ttgpcggcaca gca 617  
 Gln Ala Leu Asn Asn Leu  
 195

G10 - 78

G11 - 193

G12 - PRT

G13 - *Corynebacterium glutamicum*

G10 - 78

Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys  
 1 5 10 15  
 Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn  
 20 25 30  
 Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly  
 35 40 45  
 Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys  
 50 55 60  
 Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile  
 65 70 75 80

Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro  
 85 90 95

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys  
 100 105 110

Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala  
 115 120 125

Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser  
 130 135 140

Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His  
 145 150 155 160

Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg  
 165 170 175

Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu  
 180 185 190

Gln Ala Leu Asn Asn Leu  
 195

&lt;210&gt; C9

&lt;211&gt; (117)

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)...(1147)

&lt;223&gt; EXA02532

&lt;400&gt; C9

gatgaatttt taaccacccat ctgtacctat taaccctggc tggcgtccac ccacagtaac 60

tgtgcaagcg ggaaggccag ccaggaactcc tgggtggcgc atg aac cca cct atc 115  
 Met Asn Pro Pro Ile  
 1 5

acc ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc 163  
 Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu Lys Ala Tyr Gly Arg  
 10 15 20

gat ggc aat gat gga tgg ggt gca ttt gag gct gcc atg gga act cta 211  
 Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala Ala Met Gly Thr Leu  
 25 30 35

gat ggt gag ttc gcc gta tct tat tct tca ggt ttg gca gag gca aag 259  
 Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly Leu Ala Ala Ala Thr  
 40 45 50

tgg att gct gat ttg gtt cct act ggt ggc aca gtt gtt tta cct aaa 307  
 Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr Val Val Leu Pro Lys  
 55 60 65

gct gcc tat tat ggc gtg acc aat att ttc gcc agg atg gaa gcc cgc 355  
 Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala Arg Met Glu Ala Arg  
 70 75 80 85



gga agg ctg aag gtt cga act gtt gat gca gac aat acc gaa gaa gtg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp Asn Thr Glu Glu Val 90 95 100	403
att gct gct gct caa ggt gca gat gtg gng tgg gtg gaa tgg atc gct Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp Val Glu Ser Ile Ala 105 110 115	451
aat cgg aag atg gtg gta gct gat atc cct gca ata gtc gac ggt gtg Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala Ile Val Asp Gly Val 120 125 130	499
cgt ggg cct gga gtt tgg act gtc gct gac gog act ttc gca aag cca Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala Thr Phe Ala Thr Pro 135 140 145	547
ctt cgt caa cgt cca tgg gaa ctt ggt gct gat att gtg ctt taa tgg Leu Arg Gln Arg Pro Leu Gln Leu Gly Ala Asp Ile Val Leu Tyr Ser 150 155 160 165	595
gca acc aas ctt atc ggt gga caa cct gat ctt ctt ctt gga gtc cca Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu Leu Leu Gly Val Ala 170 175 180	643
gtg cga aag cct gag caa cat ggc cag tct ctt gcc act caa cgt cat Val Cys Lys Ser Gln His His Ala Gln Phe Leu Ala Thr His Arg His 185 190 195	691
gac cat ggt caa gtg cgg gga ggt ctt gaa gog ctt ctt gat ctc cgt Asp His Gly Ser Val Pro Gly Gly Leu Gln Ala Phe Leu Ala Leu Arg 200 205 210	739
gga tgg tat taa tgg ggc gta cgt ctt gat cga gca gaa tcc aac gca Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg Ala Glu Ser Asn Ala 215 220 225	787
gca gaa ctt tgg cgg cga ctt aac gog cat ctt tgg gtt acc cgg gtc Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro Ser Val Thr Arg Val 230 235 240 245	835
aat tat cca gga ctt ctt gat gat ccc caa cat gaa aaa gcc gtg cga Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His Glu Lys Ala Val Arg 250 255 260	883
gtc cta ccc tct gga tct gga aac atg tgg cca ttt gag ctt gat gca Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp Ala 265 270 275	931
aca cct gaa cga act gat gaa att ctc gaa agc ctg cca ctt taa acc Thr Pro Gln Arg Thr Asp Gln Ile Leu Glu Ser Leu Ser Leu Leu Thr 280 285 290	979
cac ggc acc agt tgg gga ggt gtg gaa aca gcc att gaa cgt cgc acc His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg Thr 295 300 305	1027
agg cgg gat gct gaa gtg gta gca gaa gta ccg atg act ctt tgc cgc Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro Met Thr Leu Cys Arg 310 315 320 325	1075

ggt tcc gta gga att gaa gac gtt gaa gat cta tgg gaa gac ctc aac 1123  
 Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu Asn  
                   330                  335                  340

gac tca atc gac aaa gtt ctg ggt tagaactcgt agccagtaac cag 1170  
 Ala Ser Ile Asp Lys Val Leu Gly  
                   345

(210): 80

(211): 349

(212): PRT

(213): *Corynebacterium glutamicum*

(400): 80

Met Asn Pro Pro Ile Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu  
   1                  10                  15

Lys Ala Tyr Gly Arg Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala  
                   20                  25                  30

Ala Met Gly Thr Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly  
                   35                  40                  45

Leu Ala Ala Ala Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr  
                   50                  55                  60

Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala  
                   65                  70                  75                  80

Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp  
                   85                  90                  95

Asn Thr Glu Glu Val Ile Ala Ala Ala Glu Gly Ala Asp Val Val Trp  
                   100                  105                  110

Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala  
                   115                  120                  125

Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala  
                   130                  135                  140

Thr Phe Ala Thr Pro Leu Arg Glu Arg Pro Leu Glu Leu Gly Ala Asp  
                   145                  150                  155                  160

Phe Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu  
                   165                  170                  175

Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Glu Phe Leu  
                   180                  185                  190

Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala  
                   195                  200                  205

Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg  
                   210                  215                  220

Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro  
                   225                  230                  235                  240

Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His

245	250	255
Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser		
260	265	270
Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser		
275	280	285
Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala		
290	295	300
Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro		
305	310	315
Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu		
325	330	335
Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly		
340	345	

&lt;110&gt; #1

&lt;111&gt; #61

&lt;112&gt; DNA

&lt;113&gt; Corynebacterium glutamicum

&lt;120&gt;

&lt;121&gt; CDS

&lt;122&gt; (101)...(338)

&lt;123&gt; EX303159

&lt;130&gt; #1

aggggtatgt tttaacacaaa agnaggacagc ttggttatcc atggacagaa gacgggttct 60

ctataggaca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca	115
Leu Ser Phe Asp Pro	
1	

aac acc bag ggt ttc tcc act gca tcc att cac gct ggg tat gag cca	163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro	
10 15 20	

gac gac tac tac ggt tcc att aac acc cca atc tat gcc tcc acc acc	211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr	
25 30 35	

ttc ggg bag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc	259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr	
40 45 50	

cgt gtg ggc aac ccc acc atc ggg gca tta gag cac acc gtc gca gca	307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Glu Thr Val Ala Ala	
55 60 65	

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca	355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala	
70 75 80 85	

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc	403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val	
90 95 100	

ctg ggc aac gat got tac ggc gga acc tac cgc ctg atc gac acc gta 451  
 Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val  
 105 110 115  
 ctg acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499  
 Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val  
 120 125 130  
 gaa gag gtc aag gca ggc atc aag gac aac acc aag ctg atc tgg gtg 547  
 Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Leu Ile Trp Val  
 135 140 145  
 gaa acc cca acc aac cca gca ctt ggc atc acc gac atc gaa gca gta 595  
 Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr Asp Ile Glu Ala Val  
 150 155 160 165  
 gca aac ctg acc gaa ggc acc aac ggc aag tgg gtt gtt gac aac acc 643  
 Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu Val Val Asp Asn Thr  
 170 175 180  
 ttg cca tcc cca tac ctg cag cag cca cta aaa ctg ggc gca cac gca 691  
 Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys Leu Gly Ala His Ala  
 185 190 195  
 agt cct tgc act cca cca cca agt aca tgg aag gac act ccg acc ctg 739  
 Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys Asp Thr Pro Thr Leu  
 200 205 210  
 ttg acc gac ttg tgg gta cca acc acc agg aaa tgg acc aag aac tgc 787  
 Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys Trp Thr Lys Asn Cys  
 215 220 225  
 agt tca tgc agg ggc gca tgg gac cga tcc cat cag ttt tgg atg cat 835  
 Lys Ser Cys Arg Ala Ala Ser Asp Arg Ser His Gln Phe Ser Met His  
 230 235 240 245  
 acc tgaaccgacg tggcctcaag acc 861  
 Thr

4210 - 12

4211 - 146

4212 - PRF

4213 - *Corynebacterium glutamicum*

4400 - 12

Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His  
 1 5 10 15

Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile  
 20 25 30

Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys  
 35 40 45

Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu  
 50 55 60

Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser

65	70	75	80
Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro			
	85	90	95
Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg			
	100	105	110
Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val			
	115	120	125
Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr			
	130	135	140
Lys Leu Ile Trp Val Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr			
	145	150	155
Asp Ile Glu Ala Val Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu			
	160	165	170
Val Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys			
	175	180	185
Leu Gly Ala His Ala Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys			
	190	195	200
Asp Thr Pro Thr Leu Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys			
	205	210	215
Trp Thr Lys Asn Cys Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His			
	220	225	230
Val Thr Ser Met His Thr			
	235	240	245

<210>=2  
 <210>=10  
 <210> DNA  
 <210> Corynebacterium glutamicum

<210>  
 <210> CDS  
 <210> (1..1)..(701)  
 <210> FRMAC2761

<210>  
 <210> misc\_feature  
 <210> 59-,676,687,690,691,693  
 <210> n = a, c, t, or g

<210>  
 <210> VARIANT  
 <210> 13  
 <210> Xaa = His or Gln

<210>  
 <210> VARIANT  
 <210> 190  
 <210> Xaa = Ile, Thr, Asn, or Ser

0020 -

0021 - VARIANT

0022 - 197

0023 - Kaa = Phe, Leu, Ser, Tyr, STOP CODON, Cys, or Trp

0030 -

0031 - VARIANT

0032 - 196

0033 - Kaa = Val, Ala, Glu, or Gly

0400 - 43

aggggtagt tttacacaaa agtggacagc ttgggtctatc attgccagaa gacccggtcct 60

tttagggcca tagaattctg attacaggag ttgatctacc ttc tct ttt gac cca 115  
Leu Ser Phe Asp Pro  
1 3

ttt acc cag ggt ttc tcc act gca tog att cac gct ggg tat gag cca 163  
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro  
10 15 20

gat cac tac tac ggt tog att aac acc cca atc tat gac tcc acc acc 211  
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr  
25 30 35

ttt acc cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259  
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr  
40 45 50

ttt acc ggc aac ccc acc atc gtg gca tta gac cag acc gtc gca gca 307  
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala  
55 60 65

ttt gaa ggc gca aag tat ggc cgc gca tta tcc tcc ggc atg gct gca 355  
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala  
70 75 80 85

acc gat atc ctg ttc cgc atc atc ctg aag ccc ggc gat cac atc gtc 403  
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val  
90 95 100

ttt ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451  
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val  
105 110 115

ttt acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtc 499  
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val  
120 125 130

gat gat gtc aag gca ggc atc aag gat aac acc aag gct gat ctt ggt 547  
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly  
135 140 145

gta aac ccc aac caa ccc agc act ttg gca tta ccc gac atc gaa gca 595  
Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala  
150 155 160 165

gtn tgc aaa act tca ccc gaa agg cac caa ccc caa gct tgt cgt ttg 643  
Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu  
170 175 180

aca aca cct tgg cat tcc cca tac ctg cag can cca ctt aaa ant tnn 691  
 Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa  
                   135                  190                  195

gng cac aag cag 703  
 Xaa His Thr Gln  
                   100

<210> 24  
 <211> 101  
 <212> PRT  
 <213> Corynebacterium glutamicum

<220>  
 <221> VARIANT  
 <222> 191  
 <223> Xaa = His or Gln

<230>  
 <231> VARIANT  
 <232> 196  
 <233> Xaa = Ile, Thr, Asn, or Ser

<240>  
 <241> VARIANT  
 <242> 197  
 <243> Xaa = Phe, Leu, Ser, Tyr, STOP CODON, Cys, or Trp

<250>  
 <251> VARIANT  
 <252> 198  
 <253> Xaa = Val, Ala, Glu, or Gly

<260> 24  
 Val Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His  
                   1                  5                  10                  15

Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile  
                   20                  25                  30

Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys  
                   35                  40                  45

Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu  
                   50                  55                  60

Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser  
                   65                  70                  75                  80

Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro  
                   85                  90                  95

Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg  
                   100                  105                  110

Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Gln Tyr Thr Val Val  
                   115                  120                  125

Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr  
                   130                  135                  140

Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu  
145 153 151 160

Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro  
165 170 175

Gln Ala Cys Cys Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa  
180 185 190

Pro Leu Lys Xaa Xaa Xaa His Thr Gln  
195 200

1100-65

1110-111

1120-DNA

1130-Corynebacterium glutamicum

1200-

1210-CDS

1220-1110... (1091)

1230-EXA (216)

1400-65

atgttgctat cgggcaaggca gaagtgctat aactgctga cgggcatggg gacatcgtc 60

atggatcagt caccatctga cacacgggagt attaagaaaa ttg ggc gct tat ggt 115  
Leu Gly Ala Tyr Gly  
1

tta ggt gag att att gga aaa taa ggc ggc gaa ggc ggc gac att att 163  
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Gln Ala Ala Asp Ile Ile  
10 15 20

agg ggt gag aag ggc gat att att att att att att att att att att 211  
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg  
25 30 35

ggt ttg att ggt gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259  
Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met  
40 45 50

ttc aac gtt gat cgc ggg ggc cga tct tgg gtc atg agc aca cgc ccc 307  
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro  
55 60 65

agg aga ttg aag ccc ctg acc ggc gat ttc att gac atg gat ttg gat 355  
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp  
70 75 80 85

ggg tgc gag gaa acc tgg gga acc ggc gtc gac aag cta aaa atc caa 403  
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln  
90 95 100

ttt gct ggt ccc tgg act tta ggt ggc cgc att gag ttg ggc aat ggc 451  
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly  
105 110 115

cat cgc gtt ttg tct gat cgc ggt ggc atg cgt gat ctg acc cag ggc 499  
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala



120	125	130	
ctg atc gag ggc atc gat ggg cat gca cgc aag gtt gct ggg cga ttt			547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe			
135	140	145	
ggc aac gaa gtg cag gtg caa att gat gag cgg gag ctg aaa tog ctt			595
Arg Ala Glu Val Glu Val Glu Ile Asp Glu Pro Glu Leu Lys Ser Leu			
150	155	160	165
atc aac ggc tcc ctg cct ggc aat tcc acc ttt gac att att cct gag			643
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala			
170	175	180	
gtg aat gtc gat gat gcc agt gaa cgt ttg cag cag gtc ttt agc tag			691
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Glu Glu Val Phe Ser Ser			
185	190	195	
ttc cag ggg cgg aca tat ctg aac ctg acc ggc cag att cct aat tgg			739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Glu Ile Pro Thr Trp			
200	205	210	
gat ctg gat cgg ggt gcc ggc gcc gat aat ggg cag att tcc atg gat			787
Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Glu Ile Ser Met Asp			
215	220	225	
caa ctg cct gga aat gaa cat ttg gat ggt ttc ggt gaa acc atc acc			835
Glu Val Arg Gly Asn Glu Ala Leu Asp Gly Phe Gly Glu Thr Ile Thr			
230	235	240	245
agt cga atc cgt ctt ggt ttg ggc att aag aca gga aaa gat gtc gta			883
Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val			
250	255	260	
gat caa cgg ctg gag cga cgg cgg caa aag gcc gtt gag gta gca cgc			931
Asp Glu Leu Leu Glu Arg Pro Arg Glu Lys Ala Val Glu Val Ala Arg			
265	270	275	
ttc ttc gat cgt tta ggt gtg ggc cga aac tat ctg gtc gat gat gta			979
Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val			
280	285	290	
gat att cat cgg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc			1027
Asp Ile His Pro Gly Glu Asp Leu Val Glu Gly Thr Ile Thr Glu Ala			
295	300	305	
gag cag gat tat cgc atg gcc cgg gtg atg ttg gag atg ttg tog aag			1075
Ala Glu Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys			
310	315	320	325
gat tca tgc gac ctt taaggcttta caggcgtggtg gtg			1113
Asp Ser Cys Asp Leu			
330			

1210 &gt; 86

1211 &gt; 330

1212 &gt; PBT

1213 > *Corynebacterium glutamicum*

1400 &gt; 86

Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu  
 1 5 10 15  
 Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro  
 20 25 30  
 Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val  
 35 40 45  
 Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val  
 50 55 60  
 Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu  
 65 70 75 80  
 Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp  
 85 90 95  
 Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile  
 100 105 110  
 Gln Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg  
 115 120 125  
 Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys  
 130 135 140  
 Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro  
 145 150 155 160  
 Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe  
 165 170 175  
 Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln  
 180 185 190  
 Glu Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly  
 195 200 205  
 Glu Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val  
 210 215 220  
 Glu Ile Ser Met Asp Glu Val Arg Gly Asn Glu His Leu Asp Gly Phe  
 225 230 235 240  
 Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr  
 245 250 255  
 Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala  
 260 265 270  
 Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr  
 275 280 285  
 Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly  
 290 295 300  
 Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser  
 305 310 315 320  
 Glu Met Leu Ser Lys Asp Ser Cys Asp Leu

325

330

02100 87  
 02111 551  
 0212 DNA  
 0213 Corynebacterium glutamicum

0220  
 0221 CDS  
 0222 (1)...(528)  
 0223 EXA02187

02100 87  
 ggc gaa cgc atg cgc ttt aac ttc cca cgc cag cag cgc ggc agg ttc 48  
 Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe  
 1 5 10 15  
 tgg tgc atc gag gat ttc att cgc cca cgc gag caa gct gtc aag gac 96  
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp  
 20 25 30  
 ggc gaa gtg gag gtc atg cca ttc cag ctg gtc acc atg ggt aat cct 144  
 Gly Glu Val Asp Val Met Pro Phe Glu Leu Val Thr Met Gly Asn Pro  
 35 40 45  
 att cct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag 192  
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
 50 55 60  
 tac ttg gaa gtt cac ggc aac ggc gtg cag ctg acc gaa gca tgg gcc 240  
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80  
 gag tac tgg cac tcc cga gtg cgc agc gaa ctg aag ctg aac gac ggt 288  
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95  
 ggc cct gtc ggt gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336  
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110  
 ttg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384  
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125  
 gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctg gag cca ggc cgt 432  
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg  
 130 135 140  
 atc ggc gtg gag ttg tcc gag gaa ctg cag ctg cac cca gag cag tcc 480  
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser  
 145 150 155 160  
 aca gac ggc ttt gtg ctg tac cac cca gag gca aag tac ttt aac gtc 528  
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
 165 170 175  
 taacaccttt gagagggaaa act 551

0210 - 83  
 0211 - 176  
 0212 - PRT  
 0213 - *Corynebacterium glutamicum*

0400 - 88  
 Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe  
 1 3 10 15  
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp  
 20 25 30  
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro  
 35 40 45  
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
 50 55 60  
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80  
 His Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95  
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110  
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125  
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg  
 130 135 140  
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser  
 145 150 155 160  
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
 165 170 175

0210 - 88  
 0211 - 2899  
 0212 - DNA  
 0213 - *Corynebacterium glutamicum*

0200 -  
 0201 - CDS  
 0202 - (101)..(2599)  
 0203 - EX02198

0400 - 89  
 agactagtggtt cgttttgctt gtgttgotta ggcggggttg aaaatgaact acgaatgaaa 60  
 agttcggggaa ttgtctaata cgtactaagc tgtctacaca atg tct act tca gtt 115  
 Met Ser Thr Ser Val  
 1 5  
 act tca tca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163  
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
 10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc	311
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu	
25 30 35	
caa ggc ttt gac ctg gac gtc gaa aag gat ttc ctt gat ctg gag ggg	359
Gln Gly Phe Asp Leu Asp Val Gln Lys Asp Phe Leu Asp Leu Glu Gly	
40 45 50	
tgt aat gag att ctc aac gac aac cgc cct gat gtg ttg agg cag att	367
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile	
55 60 65	
cac cgc gcc tac ttt gag gcc gga gct gac ttg gtt gag acc aat act	355
His Arg Ala Tyr Phe Gln Ala Gly Ala Asp Leu Val Gln Thr Asn Thr	
70 75 80 85	
ttt ggt tgc aac ctg ccg aac ttc ggc gat tat gac atc gct gat cgt	403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg	
90 95 100	
tgc cgt gag ctt gcc tac aag ggt act gca gtg gct agg gaa atg gct	451
Cys Arg Gln Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	
115 120 125	
gat gag atg ggc ccg gcc cca aat ggc atg cgg cgt ttc gtg gtt ggt	499
Asp Gln Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	
130 135 140	
tac ctg gga cct gga aag aag ctt cca tcc ctg cgc cat gca ccg tat	547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
145 150 155	
gca gat ttg cgt ggg cac tac aac gaa gca gcc ctt gcc atc atc gac	595
Ala Asp Leu Arg Gly His Tyr Lys Gln Ala Ala Leu Gly Ile Ile Asp	
160 165 166	
ggt ggt gcc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag	643
Gly Gly Gly Asp Ala Phe Leu Ile Gln Thr Ala Gln Asp Leu Leu Gln	
170 175 180	
gtc aag gct gcc ctt cac gcc gtt cca gat gcc atg gct gaa ctt gat	691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
185 190 195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc gcc acc	739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
200 205 210	
atg ctc atg ggt cct gag atc ggt gcc gcc ttg aca gcc ctg cag cca	787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
215 220 225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc gcc cca gat gag	835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
230 235 240 245	
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg	883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
250 255 260	
tgc gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca	931

Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu	Gly	Lys	Asn	Gly	Ala	
			265					270					275			
gaa	tac	cca	ctt	gag	gct	gag	gat	ttg	gag	cag	gag	ctg	gct	gga	ttc	979
Glu	Tyr	Pro	Leu	Glu	Ala	Glu	Asp	Leu	Ala	Gln	Ala	Leu	Ala	Gly	Phe	
		380					385					390				
gtc	ccc	aaa	tat	ggc	ctg	ccc	atg	gtg	ggt	ggt	tgt	tgt	ggc	acc	aca	1027
Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly	Cys	Cys	Gly	Thr	Thr	
	395					399					405					
ccg	gag	aac	atc	cgt	ggc	gtc	cgc	gat	ggc	gtg	gtt	ggt	gtt	cca	gag	1075
Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val	Val	Gly	Val	Pro	Glu	
310					315					320					325	
cag	gaa	acc	ccc	aca	ctg	aac	cag	atc	cat	cca	ggc	cat	gtt	gac	cag	1123
Gln	Glu	Thr	Ser	Thr	Leu	Thr	Lys	Ile	Pro	Ala	Gly	Pro	Val	Gln	Gln	
				330						335				34		
gac	ccc	agg	gag	gtc	gag	aaa	cag	gac	ccc	gtc	ggc	ccc	ctg	ccc	acc	1171
Ala	Ser	Arg	Glu	Val	Glu	Lys	Gln	Asp	Ser	Val	Ala	Ser	Leu	Tyr	Thr	
		345						350						355		
tcg	gtg	cca	tig	ccc	cag	gaa	acc	ggc	att	ccc	atg	atc	ggt	gac	cgc	1219
Ser	Val	Pro	Leu	Ser	Gln	Glu	Thr	Gly	Ile	Ser	Met	Ile	Gly	Gln	Arg	
		360						365				370				
acc	aac	ccc	aac	ggt	ccc	agg	cca	tcc	cgt	cag	cca	atg	ctg	ccc	ggc	1267
Thr	Asn	Ser	Asn	Gly	Ser	Lys	Ala	Phe	Arg	Glu	Ala	Met	Leu	Ser	Gly	
	375					380						385				
gat	tcg	aca	atg	tgt	gtg	gat	cat	gaa	agg	cag	caa	acc	ggc	gat	ggt	1315
Asp	Trp	Glu	Lys	Cys	Val	Asp	Ile	Ala	Lys	Gln	Gln	Thr	Arg	Asp	Gly	
390					395					400				405		
gca	ccc	atg	ctg	cat	ctt	ctt	agg	gat	ccc	ctg	ggc	cca	gac	ggc	acc	1363
Ala	His	Met	Leu	Asp	Leu	Cys	Val	Asp	Tyr	Val	Gly	Arg	Asp	Gly	Thr	
			41					415						420		
gac	gat	atg	ggc	acc	ctg	gaa	caa	ctt	ctt	gct	acc	agg	ccc	act	ctg	1411
Ala	Asp	Met	Ala	Thr	Leu	Ala	Ala	Leu	Leu	Ala	Thr	Ser	Ser	Thr	Leu	
			425					430					435			
cca	atc	atg	att	gac	ccc	acc	cag	cca	gag	gtt	att	ggc	aca	ggc	ctt	1459
Pro	Ile	Met	Ile	Asp	Ser	Thr	Glu	Pro	Glu	Val	Ile	Arg	Thr	Gly	Leu	
		440					445					450				
gag	ccc	ttg	ggt	gga	cca	agg	atc	gtt	aac	ccc	gtc	aac	ttt	gac	gac	1507
Glu	His	Leu	Gly	Gly	Arg	Ser	Ile	Val	Asn	Ser	Val	Asn	Phe	Gln	Asp	
	455					460					465					
ggc	gat	ggc	cat	gag	ccc	cca	tac	cag	ggc	atc	atg	aaa	ctg	gtc	aac	1555
Gly	Asp	Gly	Pro	Glu	Ser	Arg	Tyr	Gln	Arg	Ile	Met	Lys	Leu	Val	Lys	
470					475					480				485		
cag	ccc	ggt	ggc	gac	gtg	gtt	ggc	ctg	acc	att	gat	gag	gaa	ggc	cag	1603
Gln	His	Gly	Ala	Ala	Val	Val	Ala	Leu	Thr	Ile	Asp	Glu	Glu	Gly	Gln	
			490					495						500		
gca	cgt	acc	gct	gag	ccc	agg	gtg	ggc	att	gct	aaa	cca	ctg	att	gac	1651
Ala	Arg	Thr	Ala	Glu	His	Lys	Val	Arg	Ile	Ala	Lys	Arg	Leu	Ile	Asp	

505	510	515	
gat atc acc ggt agc tac ggc ctg gat atc aaa gac atc gtt gtg gac Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp 520 525 530			1699
tgc ctg acc ttc cgg atc tct act ggc cag gaa gaa acc agg cga gat Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Thr Arg Arg Asp 535 540 545			1747
ggc att gaa acc atc gaa ggc atc cgc gag ctg aag aag ctg tac cca Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro 550 555 560 565			1795
gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn 570 575 580			1843
act gct gaa ccc cag gtt ctt aac tct gtg tcc ccc aat gag tgc att Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile 585 590 595			1891
gag gct ggt ccc gac tct ggc att ggc cag aac tcc aag att ctg cgg Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro 600 605 610			1939
atg aac cgc att gat gat cgc cag cgc gaa ggt ggc ctg gat atg gtc Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val 615 620 625			1987
tat gat cgc ccc acc gag gat tac gat cgg ctg cag gaa ttc atg cag Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln 630 635 640 645			2035
cag ttc gag ggt gtt tct gct ggc gat ggc aag gat ggt tgc gct gaa Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu 650 655 660			2083
cag ctg ggc gct atg cct ctg ttc gag cgt ttg gca cag cgc atc atc Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile 665 670 675			2131
gac ggc gat aac aat ggc ctt gag gat gat ctg gaa gca ggc atg aag Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys 680 685 690			2179
gag aag tct cct att ggc atc atc aac gag gac ctt ctg aac ggc atg Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met 695 700 705			2227
aag acc gtg ggt gag ctg tct ggt tcc gga cag atg cag ctg cca ttc Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe 710 715 720 725			2275
gtg ctg cca tcc gca gaa acc atg aaa act ggc gtg ggc tac ttg gaa Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu 730 735 740			2323
cgg ttc atg gaa gag gaa gca gaa gct acc gga tct ggc cag gca gag Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu 745 750 755			2371

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat 2419  
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac 2467  
 Ile Gly Lys Asn Leu Val Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
 775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca 2515  
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
 790 795 800 805

ggg gaa gaa cac aac gaa gac gcc acc ggc atg tgg gga ctt ctt gtg 2563  
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val  
 810 815 820

aag tcc acc gtg gtc atg aag caa acc atc agc gac 2599  
 Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp  
 825 830

<310> 90

<311> 833

<312> PBT

<313> Corynebacterium glutamicum

<400> 90

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Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala  
 20 30

Met Gly Thr Glu Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe  
 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp  
 50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
 65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr  
 85 90 95

Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val  
 100 105 110

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg  
 115 120 125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu  
 130 135 140

Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala  
 145 150 155 160

Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala  
 165 170 175



Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala  
 180 185 190  
 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val  
 195 200 205  
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu  
 210 215 220  
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala  
 225 230 235 240  
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His  
 245 250 255  
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu  
 260 265 270  
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln  
 275 280 285  
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly  
 290 295 300  
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val  
 305 310 315 320  
 Val Gly Val Pro Glu Glu Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala  
 325 330 335  
 Gly Pro Val Glu Glu Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val  
 340 345 350  
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser  
 355 360 365  
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu  
 370 375 380  
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Glu  
 385 390 395 400  
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val  
 405 410 415  
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala  
 420 425 430  
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val  
 435 440 445  
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser  
 450 455 460  
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Asp Tyr Gln Arg Ile  
 465 470 475 480  
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile  
 485 490 495  
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala

500					505					510					
Lys	Arg	Leu	Ile	Asp	Asp	Ile	Thr	Gly	Ser	Tyr	Gly	Leu	Asp	Ile	Lys
515					520					525					
Asp	Ile	Val	Val	Asp	Cys	Leu	Thr	Phe	Pro	Ile	Ser	Thr	Gly	Gln	Glu
530					535					540					
Glu	Thr	Arg	Arg	Asp	Gly	Ile	Gln	Thr	Ile	Glu	Ala	Ile	Arg	Gln	Leu
545					550					555					
Lys	Lys	Leu	Tyr	Pro	Gln	Ile	His	Thr	Thr	Leu	Gly	Leu	Ser	Asn	Ile
565					570					575					
Ser	Phe	Gly	Leu	Asn	Pro	Ala	Ala	Arg	Gln	Val	Leu	Asn	Ser	Val	Phe
580					585					590					
Leu	Asn	Gln	Cys	Ile	Gln	Ala	Gly	Leu	Asp	Ser	Ala	Ile	Ala	His	Ser
595					600					605					
Ser	Lys	Ile	Leu	Pro	Met	Asn	Arg	Ile	Asp	Asp	Arg	Gln	Arg	Gln	Val
610					615					620					
Ala	Leu	Asp	Met	Val	Tyr	Asp	Arg	Arg	Thr	Glu	Asp	Tyr	Asp	Pro	Leu
625					630					635					
Gln	Gln	Phe	Met	Gln	Leu	Phe	Gln	Gly	Val	Ser	Ala	Ala	Asp	Ala	Lys
645					650					655					
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Gln	Ala	Gly	Met	Lys	Gln	Lys	Ser	Pro	Ile	Ala	Ile	Ile	Asn	Gln	Asp
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Leu	Leu	Asn	Gly	Met	Lys	Thr	Val	Gly	Gln	Leu	Phe	Gly	Ser	Gly	Gln
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Met	Gln	Leu	Pro	Phe	Val	Leu	Gln	Ser	Ala	Glu	Thr	Met	Lys	Thr	Ala
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Val	Ala	Tyr	Leu	Gln	Pro	Phe	Met	Gln	Gln	Glu	Ala	Gln	Ala	Thr	Gly
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Gly	Asp	Val	His	Asp	Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser
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Asn	Asn	Gly	Tyr	Asp	Val	Val	Asn	Leu	Gly	Ile	Lys	Gln	Pro	Leu	Ser
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 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
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 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu  
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 cca ggc ttt gac ctg gac gtg gaa aag gat tcc ctg gat ctg gag ggc 259  
 Ala Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly  
 40 45 50  
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 Pys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile  
 55 60 65  
 cca cgc gcc tac ttt gag ggc gga gct gac ctg gtt gag acc aat act 355  
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr  
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 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg  
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 Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala  
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 gat gag atg ggc cgc ggc cca aac ggc atg cgc cgt ttc gtg gtt ggt 499  
 Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly  
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 Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr  
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 gaa gat ttg cgt ggc cac ttc aag gaa gca ggc ctt ggc atc atc gac 595  
 Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp  
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Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln	
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Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
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Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
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Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
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Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
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Met Ser Glu His Leu Arg Phe Leu Ser Lys His Ala Asp Ile Pro Val	
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Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
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Glu Tyr Pro Leu Glu Ala Gln Asp Leu Ala Gln Ala Leu Ala Gly Phe	
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Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
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Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
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Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	
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Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly	
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goc gat atg gag acc ttg gaa gca ctt ctt gct acc agc tcc aat ttg	1411
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Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu	
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Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp	
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Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Gln Glu Gly Gln	
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Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp	
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Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp	
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Gln	Leu	Ala	Ala	Met	Pro	Leu	Phe	Glu	Arg	Leu	Ala	Gln	Arg	Ile	Ile		
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Pro	Phe	Met	Gln	Glu	Glu	Ala	Glu	Ala	Thr	Gly	Ser	Ala	Gln	Ala	Glu		
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Gly	Lys	Gly	Lys	Ile	Val	Val	Ala	Thr	Val	Lys	Gly	Asp	Val	His	Asp		
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Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser	Asn	Asn	Gly	Tyr	Asp		
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Ala	Glu	Glu	His	Lys	Ala	Asp	Val	Ile	Gly	Met	Ser	Gly	Leu	Leu	Val		
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aag	ccc	acc	gtg	gtg													2578
Lys	Ser	Thr	Val	Val													
			825														

C10 - 92

C11 - 816

C12 - PBT

C13 - Corynebacterium glutamicum

C100 - 92

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Met	Ala	Glu	Leu	Asp	Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val
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Thr	Gly	Pro	Asp	Glu	Met	Ser	Gln	His	Leu	Arg	Tyr	Leu	Ser	Lys	His
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Val	Asn	Phe	Glu	Asp	Gly	Asp	Gly	Pro	Glu	Ser	Arg	Tyr	Gln	Arg	Ile
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Glu	Thr	Arg	Arg	Asp	Gly	Ile	Glu	Thr	Ile	Glu	Ala	Ile	Arg	Glu	Leu
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Gln	Glu	Phe	Met	Gln	Leu	Phe	Glu	Gly	Val	Ser	Ala	Ala	Asp	Ala	Lys
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Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly 740 745 750
Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys 755 760 765
Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser 770 775 780
Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser 785 790 795 800
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K10 - 93

K11 - 621

K12 - DNA

K13 - *Corynebacterium glutamicum*

K10 -

K11 - CDS

K12 - (101) (198)

K13 - EXN03074

K4 0 - 93

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&lt;213&gt; Corynebacterium glutamicum

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1 5

caa caa ttc att gca acc gca gac ctg gta gac atc atc ggc gac aac 163  
Pro Gln Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
11 15 20

ggc caa tca tgc gac act cag ttt caa aac ctg gga ggt gct aca gaa 211  
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
25 30 35

ttc caa gga ata ata acc acc gtg aaa tgc ttc caa gac aac ggc ctg 259  
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
40 45 50

ctg caa tcc atc ctg agc gag gat aat cct ggc gga gtg ctg gtt atc 307  
Leu Lys Ser Ile Leu Ser Gln Asp Asn Pro Gly Gly Val Leu Val Ile  
55 60 65

gat agc gac gaa tcc gtg caa acc ggc ata gtt ggc gac atc att gca 355  
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
70 75 80 85

ggc ctg gga aaa gat cat ggt tgg tcc gca gta att gtc aac gga gca 403  
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
105 110 115

ctt cga acc aac cgg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
120 125 130

gac ata gtg gta tgg att ggt ggc att gac ttc att cct ggt cat tac 547  
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
135 140 145

gtc tac ggc gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
 150 155 160 165

gag taatttggtt tgaaggagca gta 621  
 Gln

02100: 96  
 02110: 166  
 02115: PET  
 02120: Corynebacterium glutamicum

02400: 96  
 Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
 1 5 10 15  
 20 Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
 25 30  
 35 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
 40 45  
 50 Lys Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Gln Asp Asn Pro Gly  
 55 60  
 65 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
 70 75 80  
 85 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
 90 95  
 100 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
 105 110  
 115 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 120 125  
 130 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
 135 140  
 145 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
 150 155 160  
 165 Gln Ala Pro Ile Lys Gln  
 165

02100: 97  
 02110: 1357  
 02115: DNA  
 02120: Corynebacterium glutamicum

02100:  
 02110: CDS  
 02115: (111) (1534)  
 02120: EXN00132

04000: 97  
 aasagcttca atcaattcgg tgtccactcc aacatgtaga gtggtgcgcg ttaaaaaagt 60

tttcttaatt ttcattttct taaaaggagc tcgpcaggac atg gca cag gtt atg	115
Met Ala Gln Val Met	
1 5	
gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag	165
Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln	
10 15 20	
att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag	211
Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys	
25 30 35	
gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt cct	259
Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser	
40 45 50	
atc cac atg aag gtc cag acc ccc gtc ctt att gag acc ctc act gct	307
Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala	
55 60 65	
tcg gcc cct gag gtt cgt tgg gcc tcc tgc aac att ttc tcc acc cag	355
Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln	
70 75 80 85	
gat gag cct gca gcc gct atc gtt gtc gcc tcc gcc acc gtc gaa gag	405
Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu	
90 95 100	
cca gct cgt gtt cca gta ttc gca tgg aag ggt gag tca ctg gag gag	451
Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu	
105 110 115	
cac tgg tgg tgc atc aac cag atc ttc agc tgg gcc gat gag ctg cca	499
Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro	
120 125 130	
aac atg atc ctc gac gac gcc ggt gac gcc acc atg gct gtt att cgc	547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg	
135 140 145	
ggt cgc gaa cac gag cag cgt ggt ctg gtt cca cca gca gag gcc aac	595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn	
150 155 160 165	
gat tcc gat gag tac atc gca ttc ctg gcc atg ctg cgt gag gtt ctt	643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu	
170 175 180	
gct gca gag cct gcc aag tgg gcc aag atc gct gag gcc gtt aag ggt	691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly	
185 190 195	
gtc acc gag gaa acc acc acc gcc gtt gtt ccc cgc ctg tac ccc ttc gct	739
Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala	
200 205 210	
gaa gaa gcc gtt ctg cct ttc cca gcc atg aac gtc aac gac gct gtc	787
Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val	
215 220 225	

acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc	835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile	
237 235 241 243	
gac ggc atc aac cgc gcc aat gac atg ctg atg ggc ggc aag aac gtg	883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val	
250 251 260	
ctt gtc tgc ggt tac ggc gat gtc gcc aag cgc tgc gct gag gct ttc	931
Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe	
265 270 275	
gac ggc cag ggc gat cgc gtc aag gtc acc aac gct gac cca atc aac	979
Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn	
281 288 291	
gct ctt cag ggt atg atg gat ggc tac tct atg gtc acc gtt gat gag	1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu	
295 300 305	
gcc atc gag gac gcc gac atc gtg atc acc cgc acc ggc aac aag gac	1075
Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp	
311 315 320 321	
atc att tcc ttc gag cag atg ctg aac atg aag gat cag gct ctg ctg	1123
Ile Ile Ser Phe Glu Gln Met Leu Lys Met Cys Asp His Ala Leu Leu	
330 335 340	
ggc aac atc ggt cag ttt gat aat gag atc gat atg cat tcc ctg ctg	1171
Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu	
345 350 355	
cac cgc gac gac gtc acc cgc acc aac atc aag ccc cag gtc gac gag	1219
His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu	
361 365 371	
ttc acc ttc tcc acc ggt cgc tcc atc atc atc ctg tcc tcc gaa ggt cgc	1267
Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg	
375 380 385	
ctg ctg aac ctt ggc aac gcc acc gaa cag cca tca ttt gtc atg tcc	1315
Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser	
390 395 400 405	
aac tct ttc gac gat cag acc att gag cag atc gaa ctg ttc caa aac	1363
Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn	
410 415 420	
gaa gga cag tcc gag aac gag gtc tac cgt atg cct aag gtt ctg gac	1411
Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp	
425 430 435	
gaa aag gtg gaa cgc atc cac gtt gag gct ttc ggc ggt cag ctg acc	1459
Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr	
440 445 450	
gaa ctg acc aag gag cag gct gag tac atc cgc gtt gac gtt gca ggc	1507
Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly	
455 460 465	
cca ttc aag cag gag cac tac cgc tac taatgattgt cagcattgag gga	1557

Pro Phe Lys Pro Glu His Tyr Arg Tyr  
470 475

0110: 98

0111: 473

0112: PRT

0113: Corynebacterium glutamicum

0400: 98

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu  
1 5 10 15

Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu  
20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala  
35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile  
50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn  
65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ile Val Val Gly Ser  
85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly  
100 105 110 115

Gln Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp  
120 125 130

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr  
135 140 145

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro  
150 155 160

Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met  
165 170 175

Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala  
180 185 190

Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg  
195 200 205

Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn  
210 215 220

Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr  
225 230 235 240

Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met  
245 250 255

Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly  
260 265 270

Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu  
275 280 285

Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val  
290 295 300

Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala  
305 310 315 320

Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys  
325 330 335

Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp  
340 345 350

Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys  
355 360 365

Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val  
370 375 380

Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro  
385 390 395 400

Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile  
405 410 415

Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu  
420 425 430

Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu  
435 440 445

Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly  
450 455 460

Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr  
465 470 475

4110-89

4111-12:

4112-DNA

4113-Corynebacterium glutamicum

4110-

4111-CDS

4112-(1...)(105)

4113-FRMA00132

4400-89

cac gtt gag ggt ctc ggc ggt cag ctc acc gaa ctg acc aag gag cag 48  
His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln  
1 5 10 15

ggt cag tac atc ggc gtt gac gtt gca ggc cca ttc aag cag gag cac 96  
Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His  
20 25 30

tac ggc tac taatgattgt cagcattgag gga 128  
Tyr Arg Tyr



35

4210 - 100

4211 - 31

4212 - PRT

4213 - *Corynebacterium glutamicum*

4400 - 100

His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln  
 1 5 10 15

Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His  
 20 25 30

Tyr Arg Tyr

35

4210 - 101

4211 - 1396

4212 - DNA

4213 - *Corynebacterium glutamicum*

4220 -

4221 - CDS

4222 - (101)..(1396)

4223 - FRXA01371

4430 - 101

taca tcttcc atcaattggg tgtcaactcc aacatctaga gtgggtggcg ctaaaaaagt 60

ttcttaatt ttatatttct taaaaggagc tggcaggagc atg gca cag gtt atg 115  
 Met Ala Gln Val Met  
 1 5

gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163  
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln  
 10 15 20

att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag 211  
 Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys  
 25 30 35

gaa ttc gca gag gag cag cct ttg aag ggc gcc cga att gct ggt tct 259  
 Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser  
 40 45 50

atc cac aig aag gtc cag acc gcc gtg ctt att gag acc ctc act gct 307  
 Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala  
 55 60 65

ttg gcc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag 355  
 Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln  
 70 75 80 85

gat gag gct gca gcc gct atc gtt gtc gcc tcc gcc acc gtc gaa gag 403  
 Asp Glu Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu  
 90 95 100

cca gct ggt gtt cca gta ttc gcc tgg aag ggt gag tca ctg gag gag 451

Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu		
			105						110								
tac	tgg	tgg	tac	ata	aac	cag	atc	ttc	agc	tgg	ggc	gat	gag	ctg	cca	499	
Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	Gly	Asp	Glu	Leu	Pro		
			120										130				
aac	atg	ata	cac	gac	gac	ggc	ggt	gac	gac	acc	atg	gct	gtt	att	ggc	547	
Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Met	Ala	Val	Ile	Arg		
			135										145				
ggt	ggc	gaa	tac	gag	cag	gct	ggt	cag	gtt	cca	cca	gca	gag	gac	aac	595	
Gly	Arg	Gln	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	Pro	Ala	Glu	Ala	Asn		
															165		
gat	tcc	gat	gag	tac	ata	gca	tcc	tac	ggc	atg	ctg	cgt	gag	gtt	ctt	643	
Asp	Ser	Asp	Gln	Tyr	Ile	Ala	Phe	Leu	Gly	Met	Leu	Arg	Glu	Val	Leu		
															180		
gct	gca	gag	cct	ggc	aag	tgg	ggc	aag	atc	gct	cag	gac	gtt	aag	ggt	691	
Ala	Ala	Gln	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Gln	Ala	Val	Lys	Gly		
															195		
gtc	acc	gag	gac	acc	acc	acc	ggt	gtg	acc	gac	ctg	tac	cac	tac	gct	739	
Val	Thr	Gln	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	His	Phe	Ala		
															210		
gaa	gaa	ggc	gtg	ctg	cct	ttc	cca	ggc	atg	acc	ctc	aac	gac	gct	gtt	787	
Glu	Glu	Gly	Val	Leu	Pro	Phe	Pro	Ala	Met	Asn	Val	Asn	Asp	Ala	Val		
															215		
acc	aag	tct	aag	ctt	gac	aac	aac	tac	ggc	acc	ggc	cac	tcc	ctg	atc	835	
Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly	Thr	Arg	His	Ser	Leu	Ile		
															240		
gac	ggc	atc	aac	ggc	gct	act	gac	atg	ctc	atg	ggc	ggc	aag	aac	gtg	883	
Asp	Gly	Ile	Asn	Arg	Ala	Thr	Asp	Met	Leu	Met	Gly	Gly	Lys	Asn	Val		
															260		
ctt	gtc	tgc	gtt	tac	ggc	gat	gtc	ggc	aag	ggc	tgc	gct	gag	gct	ttc	931	
Leu	Val	Cys	Gly	Tyr	Gly	Asp	Val	Gly	Lys	Gly	Cys	Ala	Glu	Ala	Phe		
															275		
gac	ggc	cag	gac	gct	ggc	gtc	aac	gtc	acc	caa	gct	gac	cca	atc	aac	979	
Asp	Gly	Gln	Gly	Ala	Arg	Val	Lys	Val	Thr	Gln	Ala	Asp	Pro	Ile	Asn		
															290		
gct	ctt	cag	gct	ctg	atg	gat	ggc	tac	tct	ctg	ctc	acc	gtt	gat	gag	1027	
Ala	Leu	Gln	Ala	Leu	Met	Asp	Gly	Tyr	Ser	Val	Val	Thr	Val	Asp	Glu		
															305		
gac	atc	gag	gac	ggc	gac	atc	gtg	atc	acc	ggc	acc	ggc	aac	aag	gac	1075	
Ala	Ile	Glu	Asp	Ala	Asp	Ile	Val	Ile	Thr	Ala	Thr	Gly	Asn	Lys	Asp		
															320		
atc	att	tcc	ttc	gag	cag	atg	ctc	aag	atg	aag	cat	cac	gct	ctg	ctg	1123	
Ile	Ile	Ser	Phe	Glu	Gln	Met	Leu	Lys	Met	Lys	Asp	His	Ala	Leu	Leu		
															340		
ggc	aac	atc	ggt	cac	ttt	gat	aat	gag	atc	gat	atg	cat	tcc	ctg	tgc	1171	
Gly	Asn	Ile	Gly	His	Phe	Asp	Asn	Glu	Ile	Asp	Met	His	Ser	Leu	Leu		

345	350	355	
cac cgc gac gac gtc acc cgc acc agc atc ang cca cag gtc gac gag			1219
His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu			
360	365	370	
ttc acc ttc ttc acc ggt cgc ttc atc atc gtc ctg ttc gaa ggt cgc			1267
Phe Thr Phe Ser Thr Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser			
375	380	385	
ctg ttg aac ctt ggc aac ggc acc gga cac cca tca ttt gtc atg ttc			1315
Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser			
390	395	400	405
aac tct ttc ggc gat cag acc att ggc cag atc gaa ctg ttc cca aac			1363
Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn			
410	415	420	
gaa cga cag cac gag aac gag gtc cac cgt ctg			1396
Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu			
425	430		
<210> 102			
<211> 432			
<212> PRT			
<213> Corynebacterium glutamicum			
<410> 102			
Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu			
1	1	15	1
Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu			
20	25	30	
Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala			
35	40	45	
Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile			
50	55	60	
Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn			
65	70	75	80
Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser			
85	90	95	
Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly			
100	105	110	
Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp			
115	120	125	
Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr			
130	135	140	
Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro			
145	150	155	160
Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met			
165	170	175	

Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala  
 180 185 190  
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg  
 195 200 205  
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn  
 210 215 220  
 Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr  
 225 230 235 240  
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met  
 245 250 255  
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly  
 260 265 270  
 Lys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu  
 275 280 285  
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val  
 290 295 300  
 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala  
 305 310 315 320  
 Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys  
 325 330 335  
 Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp  
 340 345 350  
 Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys  
 355 360 365  
 Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val  
 370 375 380  
 Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro  
 385 390 395 400  
 Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile  
 405 410 415  
 Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu  
 420 425 430

&lt;110&gt; 103

&lt;111&gt; 2398

&lt;112&gt; DNA

&lt;113&gt; Corynebacterium glutamicum

&lt;110&gt;

&lt;111&gt; CDS

&lt;112&gt; (101)..(2335)

&lt;113&gt; RXN02085

&lt;400&gt; 103

caaccgggtga tttagoggaac attgaaacat cgtcagaaga ttgcggtgog tccatagcggg 60  
 gatccgcacg ttoggtc-aa gcagaaagtc ttttaastcac atg act tcc aac ttt 115  
 Met Thr Ser Asn Phe  
 1 5  
 tct tcc act gtc gct ggt cct cct cgc atc gga gog aag cgt gaa ctg 163  
 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu  
 10 15 20  
 aag ttc gog ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211  
 Lys Phe Ala Leu Glu Gly Tyr Pro Asn Gly Ser Ile Glu Gly Arg Glu  
 25 30 35  
 ctt gog cag aac ggc cgc caa ttg gtc aac act gaa tgg gat tct ttg 259  
 Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu  
 40 45 50  
 tct gga ttg gat tcc gtt cag tcc gaa gga cgt tcc taa taa gaa gaa 307  
 Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala  
 55 60 65  
 atg ctc gat aac ggc gct att ttg ggt gta ctg cag gag cgt ttt gat 355  
 Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp  
 70 75 80 85  
 gac atc gct gat cat gaa aac gat ggt ctc caa ctg tgg att gaa cgc 403  
 Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg  
 90 95 100  
 taa ttt ggc gct gct ggc ggt act gag aac ctg cct gaa cag gaa atg 451  
 Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Glu Ala Met  
 105 110 115  
 aac aag tgg ttt gat aac aac taa caa taa ctc gtc cag gag ttg tct 499  
 Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser  
 120 125 130  
 gog gat aca cgt ttc gtt ttg gat gog tcc gog ctg att gag gat ctc 547  
 Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu  
 135 140 145  
 cgt tgc cag cag ggt cgt ggc gtt aat ggc cgc cct gtt ctg gtt ggt 595  
 Arg Cys Glu Glu Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly  
 150 155 160 165  
 caa ctg act ttc ctt tcc ctt gct cgc aac act gat ggt tcc aat cct 643  
 Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro  
 170 175 180  
 ttg gat caa ctg cct gaa ctg ttt gag gtc taa gag cgc ctc atc aag 691  
 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys  
 185 190 195  
 tct ttc gat act gag tgg gtt cag atc gat gag cct gog ttg gtc aac 739  
 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr  
 200 205 210  
 gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt taa aac act 787  
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr  
 215 220 225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gag ctg aac act ctt gag ggc atc ggc ctt ggc gag att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gag tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gag ggc atc gtt gat ggt cgt aac att tgg cgt	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc gac ctg tct gct gct ctt gct tcc ctg aag cgc ctg gca gct cgt	1027
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
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Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
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acc ctg gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gct	1123
Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala	
330 335 340	
ttc ggc tcc gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cca	1171
Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu	
345 350 355	
cca ggc aac atc gac ggc ggt gag ttc gat ggc gag tcc gca gca att	1219
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile	
360 365 370	
gct tct cga cgc acc tcc cca cgc acc gca cca atc acc cag gaa ccc	1267
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu	
375 380 385	
cct ggc cgt acc cgt gga tcc ttc gac act cgt gtt acc ctg cag gag	1315
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu	
390 395 400 405	
aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc	1363
Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe	
410 415 420	
cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa	1411
Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu	
425 430 435	
tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat	1459
Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp	
440 445 450	
ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac	1507
Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His	
455 460 465	

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc	1555
Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu	
476 475 430 485	
gac ggt ttc ctc cca acc gcc aac ggc tgg gtc cca agc tac ggc tcc	1603
Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser	
490 495 500	
cgc tgt gat ggt cct cca gag ttg ttc gga aac gtt tcc cgc cca gag	1651
Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala	
505 510 515	
cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag	1699
Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys	
520 525 530	
cac ttc aag gga atg ctc acc ggt cca gtc acc atc ctc gca tgg tcc	1747
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Pro Ser	
535 540 545	
tta ttc cgc gat gat cag cag ctg gat acc act gct gac cag gtt gca	1795
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala	
550 555 560 565	
ctg cca ctg agc gat gaa att aac gat ttc att gag gct ggc gcc aag	1843
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys	
570 575 580	
att ttc cag gtg gat gag cct cag att ggt gaa ctg ttg ccg cta cca	1891
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Gln Leu Leu Pro Leu Arg	
585 590 595	
gat ctc gat aag cct gcc tac ctg cag tgg tcc gtc gac tcc ttc ccc	1939
Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg	
600 605 610	
ctg cag act gcc ggc gca ccc aac gat gtc cca atc cag acc cag atg	1987
Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met	
615 620 625	
tgt tac tcc gag ttc aac gaa ctg atc tcc tgg gtc atc ggc ttg gat	2035
Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp	
630 635 640 645	
gcc cat gtc acc acc atc gaa gca gca cgt tcc gag atg cag gtc ctc	2083
Ala Asp Val Thr Thr Ile Gln Ala Ala Arg Ser Asp Met Gln Val Leu	
650 655 660	
gct gct ctg aaa tct tcc gcc ttc gag ctc ggc gtc gga cct ggt gtc	2131
Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val	
665 670 675	
tgg gat atc cag tcc ccg cgc att cct tcc ggc cag aaa gtg gac ggt	2179
Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly	
680 685 690	
ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc	2227
Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val	
695 700 705	
aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct	2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala  
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc 2323  
Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
730 735 740

gga gca act atc taaattgggt taccgctagg aac 2358  
Gly Ala Thr Ile  
745

00100: 104

00110: 745

00120: PRT

00130: Corynebacterium glutamicum

00400: 104

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly  
1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Gln Gly Tyr Trp Asn Gly Ser  
20 25 30

Ile Gln Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Gln Asn Asp Gly Leu Pro  
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
180 185 190

Gln Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
210 215 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr



225	330	235	240
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly	245	250	255
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu	260	265	270
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly	275	280	285
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys	290	295	300
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu	305	310	315
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Leu Pro Glu Val	320	325	330
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Leu Val Lys Leu	335	340	345
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala	350	355	360
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro	365	370	375
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg	380	385	390
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr	395	400	405
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Asn Ser Ala Arg Ala	410	415	420
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met	425	430	435
Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu	440	445	450
Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr	455	460	465
Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val	470	475	480
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn	485	490	495
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln	500	505	510
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr	515	520	525
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr	530	535	540
	545	550	555

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile  
565 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu  
580 590

Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser  
595 605

Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln  
610 620

Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser  
625 635 640

Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser  
645 650 655

Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly  
660 665 670

Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala  
675 680 685

Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro  
690 695 700

Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp  
705 710 715 720

Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln  
725 730 735

Ala Arg Glu Lys Ile Gly Ala Thr Ile  
740 745

0210 - 10%

0211 - 1913

0212 - tNA

0213 - Corynebacterium glutamicum

0220 -

0221 - GDS

0222 - (141)..(1900)

0223 - FEM02085

0300 - 10%

gaccgggtga tttegogaac cttgaaacat cgtcagaaga ttgccgtgag tcttagccgg 60

gctcgcagc ttccggtcaa gcagaaagtc tttaactcac atg act tcc aac ttt 115  
Met Thr Ser Asn Phe  
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163  
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu  
10 15 20

aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa cgt cgc gaa 211  
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu

	25	30	35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tgc gat tct ttg	259			
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu				
40	45	50		
tct gga ttg gat tcc gtt cag ttt gca gga cgt tcc tac tac gac gca	307			
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala				
55	60	65		
atg ctg gat acc gcc gct att ttg ggt ggc ctg cag gag cgt ttt gat	355			
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp				
70	75	80	85	
cac atc gct gat cat gaa aac gat ggt ctg cca ctg tgg att gac cgt	403			
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg				
90	95	100		
tac ttt ggc gct gct cgc ggt act gac acc ctg cat gca cag gac atc	451			
Tyr Phe Gly Ala Ala Arg Gly Thr Gln Thr Leu Pro Ala Gln Ala Met				
105	110	115		
acc aag tgg ttt gat acc aac tac cac tac ctg gtc cag gag ttg tct	499			
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser				
120	125	130		
cag gat aca cgt ttc gtt ttg gat gag tcc gcc ctg att gag gat ctg	547			
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Gln Asp Leu				
135	140	145		
agt tga cag cag gtt cgt gcc gtt aat gcc cgc cat gtt ctg gtt ggt	595			
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly				
150	155	160	165	
cca ctg act ttc ctg tcc ctg gct cgc acc act gat ggt tcc aat cct	643			
Pro Leu Thr Phe Leu Ser Leu Ala Arg Phe Thr Asp Gly Ser Asn Pro				
170	175	180		
ttg gat cac ctg cat gcc ctg ttt gag gtc tac gag cgc ctg atc aac	691			
Leu Asp His Leu Pro Ala Leu Phe Gln Val Tyr Gln Arg Leu Ile Lys				
185	190	195		
tct ttc gat act gag tgg gtt cag atc gat gag cat gcc ttg gtc acc	739			
Ser Phe Asp Thr Gln Trp Val Gln Ile Asp Gln Pro Ala Leu Val Thr				
200	205	210		
gat gtt gct cct gag gtt ttc gag cag gtc cgc gct ggt tac acc act	787			
Asp Val Ala Pro Glu Val Leu Gln Gln Val Arg Ala Gly Tyr Thr Thr				
215	220	225		
ttg gct aag cgc gat gcc gtc ttt gtc aat act tac ttc gcc tct gcc	835			
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly				
230	235	240	245	
gat cag gcc ctg aac act ctg gcc gcc atc gcc ctg gcc gcc att gcc	883			
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly				
250	255	260		
gtt gac ttg gtc acc cat gcc gtc act gag ctg gct gcc tgg aag ggt	931			
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly				
265	270	275		

gag gag ctg ctg gtt gog ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc gag ctg tgt ggt ggt ctt ggt tcc ctg aag cgc ctg gca ggt cgc	1017
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
295 300 305	
ggc cca atc gga gtg tct acc tct tgt tca ctg ctg cac gtt cct tac	1075
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
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Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala	
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Pro Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu	
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Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile	
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Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu	
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cct ggt cgt agc cgt gga tcc ttc gac act cgt gtt acc ctg cag gac	1315
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu	
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Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe	
410 415 420	
cca cag acc cca tcc att ctt tct ggt cgc ggt cgt ctg cgc aac gaa	1411
Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu	
425 430 435	
tcc atc act ttg gag cag tcc gaa gag gca atg cgc gaa gaa atc gat	1459
Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp	
440 445 450	
ctg gtc atc ggc aag cag gaa gaa ctt ggt ctt gat ctg ctg gtt cac	1507
Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His	
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ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc	1555
Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu	
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gac ggt ttc ctg tca acc ggc aac ggc tgg gtc caa agc tac ggc tcc	1603
Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser	
490 495 500	
cgc tct gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca ggc	1651
Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala	
505 510 515	

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 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
 520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc 1747  
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
 535 540 545

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 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
 550 555 560 565

ctg gca ctg ccg gat gaa att aac gat ctc atc gag gct ggc ggc aag 1843  
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 Arg Arg Arg  
 600

<210> 106

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<410> 106

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 21 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
 35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
 51 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
 65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
 85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
 101 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
 115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
 130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
 145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
 165 170 175  
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
 185 190  
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
 195 200 205  
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
 210 215 220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
 290 295 300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu Glu Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
 340 345 350  
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala  
 355 360 365  
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro  
 370 375 380  
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg  
 385 390 395 400  
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr  
 405 410 415  
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala  
 420 425 430  
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
 435 440 445  
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
 450 455 460  
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465 470 475 480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val

485	490	495
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn 501 505 510		
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln 515 520 525		
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr 530 535 540		
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr 545 550 555 560		
Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Gln Ile Asn Asp Leu Ile 565 570 575		
Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu 580 585 590		
Leu Leu Pro Ala Thr Arg Arg Arg 595 600		

&lt;110&gt; 107

&lt;111&gt; 603

&lt;112&gt; DNA

&lt;113&gt; Corynebacterium glutamicum

&lt;120&gt;

&lt;121&gt; CDS

&lt;122&gt; (100)...(180)

&lt;123&gt; FRXA12086

&lt;400&gt; 107

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Met Ser Leu Arg Phe
1 1
gag aac tct tga ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
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Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
25 30 35
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Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
40 45 50
ccc tgg gtc atc gag ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
55 60 65
cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc gcc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
70 75 80 85

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ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403  
 Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro  
                   90                  95                  100

tcc ggc cag aaa gtg gag ggt ctc ctc gag gct gca ctg cag tcc gtg 451  
 Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val  
                   105                  110                  115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cct 499  
 Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg  
                   120                  125                  130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547  
 Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala  
                   135                  140                  145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgcagg 600  
 Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile  
                   155                  160

aaa 603

<210> 103

<211> 160

<212> BRT

<213> Corynebacterium glutamicum

<4 0> 103

Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys  
                   5                  10                  15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala  
                   20                  25                  30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu  
                   35                  40                  45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr  
                   50                  55                  60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
                   65                  70                  75                  80

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His  
                   85                  90                  95

Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
                   100                  105                  110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys  
                   115                  120                  125

Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val  
                   130                  135                  140

Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile  
                   145                  150                  155                  160

<210> 109



02110-1326  
 02120- DNA  
 02130- Corynebacterium glutamicum

02200-  
 02210- CDS  
 02220- (101)..(1303)  
 02230- EXN02645

04000-109

atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa abgcgggttag agtcgaatga 60  
 aagtttgata cttctctttcg actttttagat tggattttca atg agc cag aac cgc 115  
 Met Ser Gln Asn Arg  
 1 5  
 acc agg acc act cag gtt ggt tcc ttg ccc cgt acc cca gag cta att 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
 10 15 20  
 cat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
 25 30 35  
 ttc caa att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
 40 45 50  
 aac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cag gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65  
 tcc cgt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg  
 70 75 80 85  
 ctg ggc gga ctg acc atg acc gat acc gag cgt tgg gca agc cag gaa 403  
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu  
 90 95 100  
 cca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451  
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp  
 105 110 115  
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499  
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser  
 120 125 130  
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547  
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly  
 135 140 145  
 cct att acc tac att ggc cag gaa gaa act cag acc gat gtt gat ctg 595  
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu  
 150 155 160 165  
 ctg aag aag ggc atg aac gca ggc gga gct acc gac ggc ttc gtt gca 643  
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala  
 170 175 180  
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691

Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp	
			185					190					195			
act	tat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gag	ctt	tcc	cag	gaa	739
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu	
		200					205					210				
tac	cag	atc	atc	acc	gat	gca	ggt	ctg	acc	ggt	cag	ctc	gac	gca	cag	787
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro	
	215					220					225					
gac	tig	gca	gaa	gca	tgg	gat	cag	atc	aac	cga	gag	cga	agc	gtg	aag	835
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Gln	Pro	Ser	Val	Lys	
230					235					240					245	
gat	tac	tig	gac	tgg	atc	ggt	aca	egg	atc	gat	gac	atc	aac	agt	gca	863
Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile	Asn	Ser	Ala	
			250					255						260		
gig	cag	ggc	ctt	cga	aag	gaa	cag	acc	egg	ctg	cac	atc	tgc	tgg	ggc	931
Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile	Cys	Trp	Gly	
		265					270						275			
tat	tgg	cac	gga	cga	cac	gtc	act	gac	atc	cga	ttc	ggc	gac	atc	att	979
Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly	Asp	Ile	Ile	
	280					285						290				
gat	cag	atc	ctc	cgc	gca	gag	gtc	ggc	ggc	ttc	tcc	ttc	gaa	ggc	gca	1027
Gly	His	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe	Glu	Gly	Ala	
	295					300					305					
tat	cat	cgt	cac	gca	cac	gag	tgg	cgt	ata	tgg	gaa	gaa	aac	aag	ctt	1075
Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu	Asn	Lys	Leu	
310					315					320					325	
cat	cac	ggc	tct	ggt	atc	tac	cct	ggt	ctt	gtg	tct	cac	tcc	atc	aac	1123
Pro	His	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val	Ser	His	Ser	Ile	Asn	
			330					335					340			
gat	tig	gag	cac	cga	cgc	ctg	gtt	gct	gat	cgt	atc	gtt	cag	tcc	gac	1171
Ala	Val	Glu	His	Pro	Arg	Leu	Val	Ala	Asp	Arg	Ile	Val	Gln	Phe	Ala	
			345					350					355			
cag	ctt	gtt	ggc	cct	gag	aac	gtc	att	ggc	tcc	act	gac	tgt	ggc	ctg	1219
Lys	Leu	Val	Gly	Pro	Glu	Asn	Val	Ile	Ala	Ser	Thr	Asp	Cys	Gly	Leu	
		360				365						370				
gga	gga	cgt	ctg	cat	tcc	cag	atc	gca	tgg	gca	aag	ctg	gag	tcc	cta	1267
Gly	Gly	Arg	Leu	His	Ser	Gln	Ile	Ala	Trp	Ala	Lys	Leu	Glu	Ser	Leu	
	375					380					385					
gta	gag	ggc	gct	cgc	att	gca	tca	aag	gaa	ctg	ttc	taagctagac				1313
Val	Glu	Gly	Ala	Arg	Ile	Ala	Ser	Lys	Glu	Leu	Phe					
390					395					400						
aaagagggtt	gct															1326

CL10: 110

CL11: 401

CL12: PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 111

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
 1 5 10 15  
 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30  
 Gly Glu Glu Glu Phe Phe Glu Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45  
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
 50 55 60  
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Pro Asn  
 65 70 75 80  
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
 85 90 95  
 Trp Ala Ser Gln Glu Ala Val Asn Ser Thr Pro Gly Asn Ile Glu Leu  
 100 105 110  
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
 115 120 125  
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
 130 135 140  
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Glu  
 145 150 155 160  
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
 165 170 175  
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
 180 185 190  
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
 195 200 205  
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220  
 Glu Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro  
 225 230 235 240  
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp  
 245 250 255  
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu  
 260 265 270  
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro  
 275 280 285  
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe  
 290 295 300  
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp



Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
 115 120 125

cag ttc gcc aag att gtt ggc cct gag aac gtc att ggc tcc act gac 432  
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
 130 135 140

cgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480  
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

gag tcc cta gta gag ggc ggt cgc att gca tca aag gaa ctg ttc 525  
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

taagctagac aacgagggtt gct 548

&lt;10&gt; 112

&lt;11&gt; 175

&lt;12&gt; BRT

&lt;13&gt; Corynebacterium glutamicum

&lt;400&gt; 112

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro  
 1 10 15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
 21 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
 51 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 165 170 175

&lt;210&gt; 113

&lt;211&gt; 784

&lt;212&gt; DNA

0213 - *Corynebacterium glutamicum*

0220 -

0221 - CDS

0222 - (101)..(784)

0223 - FRXA02658

0240 - 113

atgaataaaa ttccgggtgc agtgacogta ggtgaggtaa acgcgggttag agtcgaatga 60

gaatttgata ctctctttcg acttttagat tggattttca atg agc cag aac cgc 115  
Met Ser Gln Asn Arg  
1 5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
10 15 20

cat cca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
25 30 35

ttc cag att ctg cag tct tct gta gag gac gtg atc aag cgc cag gtt 259  
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
40 45 50

aac ctg ggt atc gac atc ctc aac gag ggc gaa tac ggc cac gtc acc 267  
Asp Leu Gly Ile Asp Ile Leu Asn Gln Gly Glu Tyr Gly His Val Thr  
55 60 65

ttc agt gca gtt gac ttc ggt gca tgg tgg aac tac ttc ttc acc cgc 315  
Phe Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Phe Arg  
70 75 80 85

ctc agc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403  
Leu Gly Gly Leu Phe Met Thr Asp Phe Asp Arg Trp Ala Ser Gln Glu  
90 95 100

gca ctg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451  
Ala Val Arg Ser Phe Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp  
105 110 115

cgt agc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499  
Arg Arg Asp Arg Ala Leu Phe Ser Gln Ala Tyr Gln Asp Pro Val Ser  
120 125 130

ggc atc ttc acc ggt cgc ggt tct gtg ggc aac cca gag ttc acc gga 547  
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Gln Phe Thr Gly  
135 140 145

cca att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595  
Pro Ile Thr Tyr Ile Gly Gln Glu Gln Thr Gln Thr Asp Val Asp Leu  
150 155 160 165

ctg aag aag ggc atg aac gca ggc gga gct acc gac ggc ttc gtt gca 643  
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala  
170 175 180

cca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691  
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp  
185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739  
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu  
 200 205 210

taa aag atc atc acc gat gca ggt ctg acc gtt cag ctg gac gca 784  
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala  
 215 220 225

CF10: 114

CF11: 223

CF12: FRT

CF13: *Corynebacterium glutamicum*

CG00: 114

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220

Gln Leu Asp Ala  
 225

02100- 115  
 02110- 408  
 02120- DNA  
 02130- Corynebacterium glutamicum

02200-  
 02210- 323  
 02220- (101)..(385)  
 02230- EX002233

04000- 115  
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 ctcttaacac tactgtccat atacttttga aaagggtgtca gtg acc aac gtg agc 115  
 Val Thr Asn Val Ser  
 1 5  
 aac cag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile  
 10 15 20  
 aac gct cct cag atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr  
 25 30 35  
 aac ctg gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
 40 45 50  
 aac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307  
 Tyr His Gln Ala Asp Glu Gly Val Phe Gln Phe Ile Gly Pro Leu Val  
 55 60 65  
 aac ccg cag cca gcc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
 70 75 80 85  
 aat cca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405  
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
 90 95  
 cag 408

02100- 115  
 02110- 95  
 02120- PRT  
 02130- Corynebacterium glutamicum

04000- 115  
 Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp  
 1 5 10 15  
 Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys  
 20 25 30  
 Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg  
 35 40 45  
 Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe



50	55	60
Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile		
65	70	75
Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly		
85	90	95

<110> 117  
 <111> 1827  
 <112> DNA  
 <113> Corynebacterium glutamicum

<110>  
 <111> CDS  
 <112> (101)..(1804)  
 <113> EX001128

<110> 117  
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 ctttattcgc ttcagagaca ccgtggggaag gggagcagca g'g agt aaa att tcc 115  
 Val Ser Lys Ile Ser  
 1 5  
 aac'aaa ctg aag gcc ctg acc gcg g'g ctg tct g'g acc act ctg g'g 163  
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val  
 10 15 20  
 ggt'agg tgt tcc aag ctt ccg cag aac aag gat ccg caa g'g ctg ccg 211  
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg  
 25 30 35  
 tca'att tcc ggg tcc caa agc aca caa gag ata gaa ggg ccg acc ccg 259  
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Gln Ile Ala Gly Pro Thr Pro  
 40 45 50  
 aat'caa gat ccg gat ttg ttg atc ccg ggc ttc ttc agc gaa ggt gcg 307  
 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala  
 55 60 65  
 tat'ccg act cag cag tat gaa gcg gcg aag gcg tat ctg aag gaa ggg 355  
 Tyr Pro Thr Gln Gln Tyr Gln Ala Ala Lys Ala Tyr Leu Thr Gln Gly  
 70 75 80 85  
 aag'cgc agc aag tgg aat ccg gct gcg tcc act cgt att ttg gat ccg 403  
 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg  
 90 95 100  
 att'gat ctg aac act ctg cca ggt tcc aag aat gcg gaa cga aag att 451  
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile  
 105 110 115  
 gcg'atc cgt gga aag cag gtc gga aag ttg ctg aag ggt ggc g'g tat 499  
 Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr  
 120 125 130  
 cag'ccg gag aat gcg gag ttt gaa gct gag atc aag atg cgt ccg gaa 547  
 Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu  
 135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu 150 155 160 165	595
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe 170 175 180	643
gat cct tct ggc cag gtg tgg gtg ggg gat ccg cgt tgg ttg ttc aat Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn 185 190 195	691
gag tgg cag tgg atg tcc acg gtg ctg atg gcc cct ctg gtt aat ggt Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly 200 205 210	739
cct tgg ccg gca att cct cct ggt gtc gtc aat cag ctg tcc acg gat Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp 215 220 225	787
ggc tgg ttc gtg ggc ttc aat gat ggc cag tat cag ttc act ggt ttg Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu 230 235 240 245	835
gga aat ttg gat gat gat ggc cgt ttc cgt ttc gcc gcc cag gcc gtg Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val 250 255 260	883
tgg acg ttg ggc cat gct gat gtc gca ggc ccc tac act ttg gtc gct Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala 265 270 275	931
gac ggc ggc cag ttg ctg tgg gag ttc cca acg ctc acc acc gat gac Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp 280 285 290	979
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu 295 300 305	1027
ttt ggc ttg cag gat gga tgg ttg tcc agc gtc agt tcc ggc aat gtg Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val 310 315 320 325	1075
agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca ggc Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala 330 335 340	1123
att tcc tcc tcc gcc aat gtg gtg gca ggc gta cgc cac gaa aac aac Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn 345 350 355	1171
gag gca gtg ctt act gtt ggc tcc atc gaa gcc gtg act tca gat ggc Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala 360 365 370	1219
ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac ggc tgg agt Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser 375 380 385	1267

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc goa oga 1315  
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg  
 391 395 400 405  
 tgg goa aca acc ggt gag ctg gtc bag acg gag gcg gag att gtg ctg 1363  
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Gln Ala Gln Ile Val Leu  
 410 415 420  
 oca agg gat ctg acg ggt ccg atc tct gaa ttc caa ctg tca cga act 1411  
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr  
 425 430 435  
 tgg gtc cgg gcc gcc atg att att gaa ggc aag gtg tac gtg ggc gtc 1439  
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val  
 440 445 450  
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 Val Thr Arg Pro Gly Pro Gly Gln Arg Arg Val Thr Asn Ile Thr Glu  
 455 460 465  
 ttc gcg ccg agc ttg gcc gcc ggc ggc ctg tgg atc aac tgg ccg oca 1555  
 Val Ala Pro Ser Leu Gly Gln Ala Ala Leu Ser Ile Asn Trp Arg Pro  
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 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp  
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 Arg Val Gln Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn  
 505 510 515  
 ttc agt gcc ccg gtg ctg gcc gtg gca agt tcc gcc acc acc gtc tac 1699  
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr  
 520 525 530  
 ttc act gat tcc cat gcc atg ctt cag ctg ccg act gcc gat aat gat 1747  
 Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp  
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 att tgg ccg cag gtg gcc ggt ttg ctg gcc aag cgt gcc ggc ccg gtg 1795  
 Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val  
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 ttt gcc tac tgatggagct gttcttcccg cgc 1827  
 Val Ala Tyr

0110: 113

0111: 563

0112: PRT

0213: Corynebacterium glutamicum

0400: 113

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser  
1 5 10 15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp  
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile  
 35 40 45  
 Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
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 Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
 65 70 75 80  
 Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
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 Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
 100 105 110  
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
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 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
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 Thr Met Arg Arg Gln Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
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 Gly Ile Leu Leu Gln Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
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 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
 180 185 190  
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
 195 200 205  
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
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 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240  
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 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
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 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly

355	360	365
Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe		
370	375	380
Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro		
385	390	395
Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu		
405	410	415
Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe		
420	425	430
Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys		
435	440	445
Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val		
450	455	460
Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser		
465	470	475
Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro		
485	490	495
Gln Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser		
500	505	510
Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser		
515	520	525
Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro		
530	535	540
Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr		
545	550	555
Asp Ala Ala Pro Val Val Ala Tyr		
565		

1310-119

1311-1344

1312- DNA

1313- Corynebacterium glutamicum

1310-

1311- CDS

1312- (101)..(1311)

1313- EXA02240

1400-119

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agagattatt atttctaaact tottcgaaaag aagggtattt gtc gct cag cca acc 115  
Val Ala Gln Pro Thr  
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gac gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163  
Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp



acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat 931  
 Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His  
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ggt cgt gga gca ttc tcc ggt aag gat cca agc aag gtg gac cgc tct 979  
 Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser  
 280 285 290

ggt cca tac gcc atg cgt tgg gta gca aag aac atc gtg gca gca ggc 1027  
 Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly  
 295 300 305

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 Ser Ala Asp Arg Ala Glu Val Ser Val Ala Tyr Ala Ile Gly Arg Ala  
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 Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly  
 330 335 340

atg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg 1171  
 Ser Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu  
 345 350 355

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 Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr  
 360 365 370

gct caa act gct gcc tac ggc cag ttt ggt cgc acc gat ttg gac ctt 1267  
 Ala Asp Thr Ala Ala Tyr His Phe Gly Arg Thr Asp Leu Asp Leu  
 375 380 385

att agc gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag 1315  
 Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys  
 390 395 400 405

ttg cca caaaaattcg atgtagtacc ctc 1344  
 Leu Ala

4010-120

4011-407

4012-BRT

4013-Corynebacterium glutamicum

4400-120

Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr  
 1 5 10 15

Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu  
 20 25 30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr  
 35 40 45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser  
 50 55 60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile

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Gly Phe Asn Ser Ser Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val						
		85		90		95
Ser Val Ser Ile Gly Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp						
		100		105		110
Asn Ser Asp Glu Ala Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg						
		115		120		125
Ala Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu						
		130		135		140
Thr Glu Glu Tyr Met Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser						
		145		150		155
Arg Arg Leu Thr Gln Val Arg Lys Glu Gly Ile Val Pro His Leu Arg						
		160		165		170
Pro Asp Gly Lys Thr Gln Val Thr Phe Ala Tyr Asp Ala Glu Asp Arg						
		175		180		185
Pro Ser His Leu Asp Thr Val Val Ile Ser Thr Gln His Asp Pro Glu						
		190		195		200
Val Asp Arg Ala Trp Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp						
		205		210		215
Trp Val Ile Lys Asp Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile						
		220		225		230
Thr Val Leu Ile Asn Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met						
		235		240		245
Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly						
		250		255		260
Gly Met Ala Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser						
		265		270		275
Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn						
		280		285		290
Ile Val Ala Ala Gly Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr						
		295		300		305
Ala Ile Gly Arg Ala Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp						
		310		315		320
Thr Asn Lys Glu Gly Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu						
		325		330		335
Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu						
		340		345		350
Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg						
		355		360		365
Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu						
		370		375		380
Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu						
		385		390		395
						400



Arg Ala Ala Leu Lys Leu Ala  
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<220>  
<223> Description of Artificial Sequence: primer

<400> 121  
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<210> 122  
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<220>  
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<210> 124  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 124  
gtaaaaacgac ggccagt 17

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